

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2004, 09:06:30 ; Search time 54 Seconds
(without alignments)
31.394 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	2	AAR43703 HIV-1 gp1
2	35	100.0	6	2	AAR68698 Katinger'
3	35	100.0	6	2	AAR92010 HIV-1 gp4
4	35	100.0	6	2	AAR25868 HIV-1 gp4
5	35	100.0	6	2	AAW53143 HIV gp41-
6	35	100.0	6	2	AAW67384 katinger'
7	35	100.0	6	2	AAW99905 HIV-1 vac
8	35	100.0	6	2	AAW39717 HIV-1 chim
9	35	100.0	6	3	AAW57748 Peptide a
10	35	100.0	6	3	AAW24104 HIV-1 gp4
11	35	100.0	6	4	AAW63933 Amino aci
12	35	100.0	6	4	AAW92333 Virus rel
13	35	100.0	6	4	AAW65282 HIV-1 iso
14	35	100.0	6	4	AAW98918 HIV epito
15	35	100.0	6	4	AAW63974 Amino aci
16	35	100.0	6	5	ABW07403 HIV-1 gp4
17	35	100.0	6	5	ABW14868 HIV epito
18	35	100.0	6	6	ABR39670 HIV-1 gp4
19	35	100.0	6	7	ABR62944 HIV-1 vir
20	35	100.0	6	7	ADC79307 HIV-1 gp4
21	35	100.0	7	2	AAW71631 HIV-1 gp4
22	35	100.0	7	2	AAW94444 HIV-1 gp4
23	35	100.0	7	2	AAW25897 Peptide c
24	35	100.0	7	2	AAW67413 HIV-1 gp4
25	35	100.0	7	2	AAW99911 HIV-1 vac

26	35	100.0	7	2	AAW39741 HIV1 chim
27	35	100.0	7	3	AAB29401 HIV-1 env
28	35	100.0	7	4	AAU70190 P3 peptid
29	35	100.0	7	4	AAG63975 Amino aci
30	35	100.0	7	5	AAU80301 HIV-1 can
31	35	100.0	7	5	AAU99586 Epitope o
32	35	100.0	7	5	AAU97480 HIV-1 inf
33	35	100.0	7	6	ABR39671 HIV-1 gp4
34	35	100.0	7	7	ABR62950 HIV-1 vir
35	35	100.0	7	7	ABR62947 HIV-1 vir
36	35	100.0	8	2	AAW71632 HIV-1 gp4
37	35	100.0	8	2	AAW05254 MN-HIV gp
38	35	100.0	8	4	ABP12065 HIV A02 s
39	35	100.0	8	4	ABP12063 HIV A02 s
40	35	100.0	8	4	ABP15180 HIV A24 s
41	35	100.0	8	4	ABP20177 HIV A03 m
42	35	100.0	8	5	AAU97481 HIV-1 inf
43	35	100.0	8	7	ABR62953 HIV-1 vir
44	35	100.0	9	2	AAW71637 Immunizat
45	35	100.0	9	2	AAW99914 HIV-1 vac
46	35	100.0	9	4	ABP20096 HIV A03 m
47	35	100.0	9	4	ABP15290 HIV A24 s
48	35	100.0	9	4	ABP12211 HIV A02 s
49	35	100.0	9	4	ABP18573 HIV B62 s
50	35	100.0	10	3	ABP38721 HIV-1 pep
51	35	100.0	10	3	ABP38723 HIV-1 pep
52	35	100.0	10	3	ABP38722 HIV-1 pep
53	35	100.0	10	4	ABP12372 HIV A02 s
54	35	100.0	10	4	ABP15481 HIV A24 s
55	35	100.0	10	4	ABP11618 HIV A01 s
56	35	100.0	10	4	ABP15479 HIV A01 s
57	35	100.0	10	4	ABP11616 HIV A01 s
58	35	100.0	10	4	ABP15483 HIV A24 s
59	35	100.0	10	4	ABP15393 HIV A24 s
60	35	100.0	10	5	AAU87761 HIV-1 epi
61	35	100.0	10	5	AAU93905 HIV-1 gp4
62	35	100.0	10	6	ABU70159 Human imm
63	35	100.0	10	6	ABU69713 Human imm
64	35	100.0	10	6	ABU70138 Human imm
65	35	100.0	10	6	ABU70086 Human imm
66	35	100.0	10	7	ADD96692 HIV-1 cro
67	35	100.0	10	7	ADD96619 HIV-1 cro
68	35	100.0	10	7	ADD96246 HIV-1 cro
69	35	100.0	10	7	ADD96671 HIV-1 cro
70	35	100.0	11	2	AAW99913 HIV-1 vac
71	35	100.0	11	3	AAW38671 HIV-1 pep
72	35	100.0	11	4	ABP18579 HIV B62 s
73	35	100.0	11	4	ABP18554 HIV B62 s
74	35	100.0	11	4	ABP12499 HIV A02 s
75	35	100.0	11	4	ABP12498 HIV A02 s
76	35	100.0	12	2	AAW64374 DP-178 ho
77	35	100.0	12	2	AAW99912 HIV-1 vac
78	35	100.0	12	2	AAW31961 Side-chai
79	35	100.0	12	3	AAW88866 Core poly
80	35	100.0	12	3	AAW14647 HIV-1 iso
81	35	100.0	12	3	AAW52664 T20/DP178
82	35	100.0	12	3	AAW52709 T20/DP178
83	35	100.0	12	4	AAW54911 Anti-HIV
84	35	100.0	12	4	AAW77221 Core poly
85	35	100.0	12	4	ABW00225 Viral DP1
86	35	100.0	12	4	ABW01692 Viral cor
87	35	100.0	12	4	AAU12774 DP178-lik
88	35	100.0	12	5	AAE01712 Hybrid po
89	35	100.0	12	6	ABR39672 HIV-1 gp4
90	35	100.0	12	7	ABR62958 Anti-HIV-
91	35	100.0	13	2	AAW71639 Chimeric
92	35	100.0	13	2	AAW64375 DP-178 ho
93	35	100.0	13	2	AAW92001 HIV-1 gp4
94	35	100.0	13	2	AAW31962 Side-chai
95	35	100.0	13	3	AAW89170 Core poly
96	35	100.0	13	3	AAW88910 Core poly
97	35	100.0	13	3	AAW88865 Core poly
98	35	100.0	13	3	AAW89169 Core poly

245	35	100.0	17	2	AAR68690	Aar68690 CLTB-97A	318	35	100.0	20	4	AAB77062	Aab77062 Core poly
246	35	100.0	17	2	AAR64379	Aar64379 DP-178 ho	319	35	100.0	20	4	AAB77783	Aab77783 Core poly
247	35	100.0	17	2	AAW19023	Aaw19023 HIV envel	320	35	100.0	20	4	ABB00790	Abb00790 Viral DP1
248	35	100.0	17	2	AAW25860	Aaw25860 HIV-1 T/B	321	35	100.0	20	4	ABB02266	Abb02266 Viral cor
249	35	100.0	17	2	AAW67376	Aaw67376 HIV-1 pep	322	35	100.0	20	4	ABB01531	Abb01531 Viral cor
250	35	100.0	17	2	AAW99909	Aaw99909 HIV-1 vac	323	35	100.0	20	4	ABB00066	Abb00066 Viral DP1
251	35	100.0	17	2	AAW39709	Aaw39709 HIV1 chim	324	35	100.0	20	4	AAU12615	Aau12615 DP178-lik
252	35	100.0	17	2	AAW31972	Aaw31972 Side-chai	325	35	100.0	20	4	AAU13336	Aau13336 DP178-lik
253	35	100.0	17	3	AAW88861	Aaw88861 Core poly	326	35	100.0	20	5	AAO18824	Aao18824 HIV gp41
254	35	100.0	17	3	AAW14652	Aaw14652 HIV-1 iso	327	35	100.0	20	5	ADE01551	Ade01551 Hybrid po
255	35	100.0	17	3	AAW52704	Aaw52704 T20/DP178	328	35	100.0	20	5	ADE02286	Ade02286 Hybrid po
256	35	100.0	17	3	AAW52669	Aaw52669 T20/DP178	329	35	100.0	20	6	ABR39655	Abr39655 HIV-1 gp4
257	35	100.0	17	4	AAW54916	Aaw54916 Anti-HIV	330	35	100.0	20	6	ABR39673	Abr39673 HIV-1 gp4
258	35	100.0	17	4	AAW77217	Aaw77217 Core poly	331	35	100.0	21	2	AAU13068	Aau13068 HIV647 fu
259	35	100.0	17	4	ABW01687	Abw01687 Viral cor	332	35	100.0	21	2	AAU13068	Aau13068 Side-chai
260	35	100.0	17	4	ABW00221	Abw00221 Viral DP1	333	35	100.0	21	2	AAU13068	Aau13068 Side-chai
261	35	100.0	17	4	AAW63978	Aaw63978 Amino aci	334	35	100.0	21	3	AAU13068	Aau13068 Side-chai
262	35	100.0	17	4	AAU12770	Aau12770 DP178-lik	335	35	100.0	21	3	AAU13068	Aau13068 Side-chai
263	35	100.0	17	5	AAW01708	Aaw01708 Hybrid po	336	35	100.0	21	3	AAU13068	Aau13068 Side-chai
264	35	100.0	18	2	AAW68686	Aaw68686 CLTB-94 B	337	35	100.0	21	3	AAU13068	Aau13068 Side-chai
265	35	100.0	18	2	AAW64380	Aaw64380 DP-178 ho	338	35	100.0	21	3	AAU13068	Aau13068 Side-chai
266	35	100.0	18	2	AAW25856	Aaw25856 HIV-1 T/B	339	35	100.0	21	3	AAU13068	Aau13068 Side-chai
267	35	100.0	18	2	AAW67372	Aaw67372 HIV-1 pep	340	35	100.0	21	3	AAU13068	Aau13068 Side-chai
268	35	100.0	18	2	AAW99907	Aaw99907 HIV-1 vac	341	35	100.0	21	3	AAU13068	Aau13068 Side-chai
269	35	100.0	18	2	AAW39705	Aaw39705 HIV1 chim	342	35	100.0	21	4	AAU13068	Aau13068 Side-chai
270	35	100.0	18	2	AAW31970	Aaw31970 Side-chai	343	35	100.0	21	4	AAU13068	Aau13068 Side-chai
271	35	100.0	18	3	AAW88747	Aaw88747 Core poly	344	35	100.0	21	4	AAU13068	Aau13068 Side-chai
272	35	100.0	18	3	AAW88653	Aaw88653 Core poly	345	35	100.0	21	4	AAU13068	Aau13068 Side-chai
273	35	100.0	18	3	AAW88706	Aaw88706 Core poly	346	35	100.0	21	4	AAU13068	Aau13068 Side-chai
274	35	100.0	18	3	AAW14653	Aaw14653 HIV-1 iso	347	35	100.0	21	4	AAU13068	Aau13068 Side-chai
275	35	100.0	18	3	AAW52670	Aaw52670 T20/DP178	348	35	100.0	21	4	AAU13068	Aau13068 Side-chai
276	35	100.0	18	3	AAW52703	Aaw52703 T20/DP178	349	35	100.0	21	4	AAU13068	Aau13068 Side-chai
277	35	100.0	18	4	AAW54917	Aaw54917 Anti-HIV	350	35	100.0	21	4	AAU13068	Aau13068 Side-chai
278	35	100.0	18	4	AAW77102	Aaw77102 Core poly	351	35	100.0	21	4	AAU13068	Aau13068 Side-chai
279	35	100.0	18	4	AAW77008	Aaw77008 Core poly	352	35	100.0	21	4	AAU13068	Aau13068 Side-chai
280	35	100.0	18	4	AAW77061	Aaw77061 Core poly	353	35	100.0	21	4	AAU13068	Aau13068 Side-chai
281	35	100.0	18	4	ABB00106	Abb00106 Viral DP1	354	35	100.0	21	4	AAU13068	Aau13068 Side-chai
282	35	100.0	18	4	ABB00012	Abb00012 HIV-1 gp4	355	35	100.0	21	4	AAU13068	Aau13068 Side-chai
283	35	100.0	18	4	ABB02923	Abb02923 Viral cor	356	35	100.0	21	4	AAU13068	Aau13068 Side-chai
284	35	100.0	18	4	ABB01530	Abb01530 Viral cor	357	35	100.0	21	5	AAU13068	Aau13068 Side-chai
285	35	100.0	18	4	ABB01571	Abb01571 Viral cor	358	35	100.0	21	5	AAU13068	Aau13068 Side-chai
286	35	100.0	18	4	ABB00065	Abb00065 Viral DP1	359	35	100.0	21	5	AAU13068	Aau13068 Side-chai
287	35	100.0	18	4	ABB01476	Abb01476 HIV-1 tra	360	35	100.0	21	5	AAU13068	Aau13068 Side-chai
288	35	100.0	18	4	AAU12655	Aau12655 DP178-lik	361	35	100.0	22	2	AAU13068	Aau13068 Side-chai
289	35	100.0	18	4	AAU12561	Aau12561 DP178-lik	362	35	100.0	22	3	AAU13068	Aau13068 Side-chai
290	35	100.0	18	4	AAU12614	Aau12614 DP178-lik	363	35	100.0	22	3	AAU13068	Aau13068 Side-chai
291	35	100.0	18	5	AAW01496	Aaw01496 Hybrid po	364	35	100.0	22	3	AAU13068	Aau13068 Side-chai
292	35	100.0	18	5	AAW01591	Aaw01591 Hybrid po	365	35	100.0	22	3	AAU13068	Aau13068 Side-chai
293	35	100.0	18	5	AAW01550	Aaw01550 Hybrid po	366	35	100.0	22	3	AAU13068	Aau13068 Side-chai
294	35	100.0	19	2	AAW64381	Aaw64381 DP-178 ho	367	35	100.0	23	2	AAU13068	Aau13068 Side-chai
295	35	100.0	19	2	AAW31963	Aaw31963 Side-chai	368	35	100.0	23	2	AAU13068	Aau13068 Side-chai
296	35	100.0	19	3	AAW14654	Aaw14654 HIV-1 iso	369	35	100.0	23	2	AAU13068	Aau13068 Side-chai
297	35	100.0	19	3	AAW52702	Aaw52702 T20/DP178	370	35	100.0	23	2	AAU13068	Aau13068 Side-chai
298	35	100.0	19	3	AAW52671	Aaw52671 T20/DP178	371	35	100.0	23	2	AAU13068	Aau13068 Side-chai
299	35	100.0	19	4	AAW54918	Aaw54918 Anti-HIV	372	35	100.0	23	2	AAU13068	Aau13068 Side-chai
300	35	100.0	20	2	AAW03896	Aaw03896 HIV-antib	373	35	100.0	23	2	AAU13068	Aau13068 Side-chai
301	35	100.0	20	2	AAW68684	Aaw68684 CLTB-92A	374	35	100.0	23	3	AAU13068	Aau13068 Side-chai
302	35	100.0	20	2	AAW64382	Aaw64382 DP-178 ho	375	35	100.0	23	3	AAU13068	Aau13068 Side-chai
303	35	100.0	20	2	AAW08065	Aaw08065 HIV pepti	376	35	100.0	23	3	AAU13068	Aau13068 Side-chai
304	35	100.0	20	2	AAW08066	Aaw08066 HIV pepti	377	35	100.0	23	3	AAU13068	Aau13068 Side-chai
305	35	100.0	20	2	AAW07920	Aaw07920 gp41 pept	378	35	100.0	23	3	AAU13068	Aau13068 Side-chai
306	35	100.0	20	2	AAW25854	Aaw25854 HIV-1 T/B	379	35	100.0	23	3	AAU13068	Aau13068 Side-chai
307	35	100.0	20	2	AAW67370	Aaw67370 HIV-1 pep	380	35	100.0	23	4	AAU13068	Aau13068 Side-chai
308	35	100.0	20	2	AAW99906	Aaw99906 HIV-1 vac	381	35	100.0	23	4	AAU13068	Aau13068 Side-chai
309	35	100.0	20	2	AAW39703	Aaw39703 HIV1 chim	382	35	100.0	23	4	AAU13068	Aau13068 Side-chai
310	35	100.0	20	2	AAW31969	Aaw31969 Side-chai	383	35	100.0	23	5	AAU13068	Aau13068 Side-chai
311	35	100.0	20	2	AAW31958	Aaw31958 Side-chai	384	35	100.0	23	5	AAU13068	Aau13068 Side-chai
312	35	100.0	20	3	AAW88707	Aaw88707 Core poly	385	35	100.0	23	5	AAU13068	Aau13068 Side-chai
313	35	100.0	20	3	AAW89382	Aaw89382 Core poly	386	35	100.0	23	6	AAU13068	Aau13068 Side-chai
314	35	100.0	20	3	AAW14655	Aaw14655 HIV-1 iso	387	35	100.0	24	2	AAU13068	Aau13068 Side-chai
315	35	100.0	20	3	AAW52672	Aaw52672 T20/DP178	388	35	100.0	24	2	AAU13068	Aau13068 Side-chai
316	35	100.0	20	3	AAW52701	Aaw52701 T20/DP178	389	35	100.0	24	2	AAU13068	Aau13068 Side-chai
317	35	100.0	20	4	AAW54919	Aaw54919 Anti-HIV	390	35	100.0	24	2	AAU13068	Aau13068 Side-chai

391	35	100.0	24	2	Aaw67380	HIV-1 pep	464	35	100.0	28	4	ABB01704	Abb01704	Viral cor
392	35	100.0	24	2	Aaw9984	HIV-1 vac	465	35	100.0	28	4	ABB01705	Abb01705	Viral cor
393	35	100.0	24	2	Aay39713	HIV-1 chim	466	35	100.0	28	4	ABB00379	Abb00379	Viral cor
394	35	100.0	24	3	Aay89379	Core poly	467	35	100.0	28	4	ABB01853	Abb00376	Viral cor
395	35	100.0	24	3	Aay89378	Core poly	468	35	100.0	28	4	ABB00376	Abb01850	Viral cor
396	35	100.0	24	3	Aab14659	HIV-1 iso	469	35	100.0	28	4	ABB01850	Aau12780	Dp178-lik
397	35	100.0	24	3	Aab52676	T20/Dp178	470	35	100.0	28	4	AAU12780	Aau12925	Dp178-lik
398	35	100.0	24	3	Aab52697	T20/Dp178	471	35	100.0	28	4	AAU12925	Aau12928	Dp178-lik
399	35	100.0	24	3	Aab52697	T20/Dp178	472	35	100.0	28	4	AAU12928	Aao14883	HIV epit
400	35	100.0	24	3	Aab54923	Anti-HIV	473	35	100.0	28	5	AAO14883	Aao14876	HIV epit
401	35	100.0	24	4	Aab77779	Core poly	474	35	100.0	28	5	AAO14876	Aao14897	HIV epit
402	35	100.0	24	4	Aab77779	Core poly	475	35	100.0	28	5	AAO14897	Ade01725	Hybrid po
403	35	100.0	24	4	Aab77779	Core poly	476	35	100.0	28	5	ADE01725	Ade01870	Hybrid po
404	35	100.0	24	4	AAB02262	Viral cor	477	35	100.0	28	5	ADe01870	Ade01724	Hybrid po
405	35	100.0	24	4	ABB00787	Viral Dp1	478	35	100.0	28	5	ADe01873	Ade01724	Hybrid po
406	35	100.0	24	4	ABB00786	Viral cor	479	35	100.0	28	5	ADe01873	Ade01724	Hybrid po
407	35	100.0	24	4	AAB00786	Viral cor	480	35	100.0	28	5	ADe01873	Ade01724	Hybrid po
408	35	100.0	24	4	AU13333	Dp178-lik	481	35	100.0	28	6	ABO10317	Abo10318	HIV-1 BRU
409	35	100.0	24	5	ABE07376	ELDKWA ep	482	35	100.0	29	2	AAR77742	Aar77742	p24E/CLTB
410	35	100.0	24	5	ADE02283	Hybrid po	483	35	100.0	29	2	AAR7742	Aar7742	p24E/CLTB
411	35	100.0	24	5	ADE02282	Hybrid po	484	35	100.0	29	2	AAR7742	Aar7742	p24E/CLTB
412	35	100.0	25	2	AAR7746	T1/Kating	485	35	100.0	29	3	AAB23554	Aab23554	HIV-1 der
413	35	100.0	25	2	AAR64387	DP-178 ho	486	35	100.0	29	3	AAB23554	Aab23554	HIV-1 der
414	35	100.0	25	3	AAB14660	HIV-1 iso	487	35	100.0	29	3	AAB23554	Aab23554	HIV-1 der
415	35	100.0	25	3	AAB52677	T20/Dp178	488	35	100.0	29	3	AAB23554	Aab23554	HIV-1 der
416	35	100.0	25	3	AAB52696	T20/Dp178	489	35	100.0	29	3	AAB23554	Aab23554	HIV-1 der
417	35	100.0	25	4	AAB54924	Anti-HIV	490	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
418	35	100.0	26	2	AAR77744	p24E/CLTB	491	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
419	35	100.0	26	2	AAR68693	p24E/CLTB	492	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
420	35	100.0	26	2	AAR64388	DP-178 ho	493	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
421	35	100.0	26	2	AAB25863	HIV-1 T/B	494	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
422	35	100.0	26	2	AAB67379	HIV-1 pep	495	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
423	35	100.0	26	2	AAB59983	HIV-1 vac	496	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
424	35	100.0	26	3	AAY8709	Core poly	497	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
425	35	100.0	26	3	AAB14661	HIV-1 iso	498	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
426	35	100.0	26	3	AAB52678	T20/Dp178	499	35	100.0	29	4	AAB23554	Aab23554	HIV-1 der
427	35	100.0	26	3	AAB52695	T20/Dp178	500	35	100.0	29	5	ADE02128	Ade02128	Hybrid po
428	35	100.0	26	4	AAB54925	Anti-HIV								
429	35	100.0	26	4	AAB77064	Core poly								
430	35	100.0	26	4	ABB00068	Viral cor								
431	35	100.0	26	4	ABB01533	Viral cor								
432	35	100.0	26	4	ABB01533	Viral cor								
433	35	100.0	26	4	AAU12617	Dp178-lik								
434	35	100.0	26	5	AAO18822	HIV gp41								
435	35	100.0	26	5	ADE01553	Hybrid po								
436	35	100.0	27	2	AAR03968	HIV-antib								
437	35	100.0	27	2	AAR68692	p24E/CLTB								
438	35	100.0	27	2	AAR64389	DP-178 ho								
439	35	100.0	27	2	AAR5862	HIV-1 T/B								
440	35	100.0	27	2	AAB52678	HIV-1 pep								
441	35	100.0	27	2	AAB59982	HIV-1 vac								
442	35	100.0	27	2	AAY39711	HIV1 chim								
443	35	100.0	27	3	AAB23711	HIV-1 der								
444	35	100.0	27	3	AAB14662	HIV-1 iso								
445	35	100.0	27	3	AAB52679	T20/Dp178								
446	35	100.0	27	3	AAB52694	T20/Dp178								
447	35	100.0	27	3	AAB38649	HIV-1 pep								
448	35	100.0	27	4	AAB54926	Anti-HIV								
449	35	100.0	27	5	AAO14881	HIV epit								
450	35	100.0	28	2	AAR77743	p24E/CLTB								
451	35	100.0	28	2	AAR64390	DP-178 ho								
452	35	100.0	28	3	AAY89020	Core poly								
453	35	100.0	28	3	AAY88872	Core poly								
454	35	100.0	28	3	AAY89017	Core poly								
455	35	100.0	28	3	AAB23557	HIV-1 der								
456	35	100.0	28	3	AAB14663	HIV-1 iso								
457	35	100.0	28	3	AAB52680	T20/Dp178								
458	35	100.0	28	3	AAB52693	T20/Dp178								
459	35	100.0	28	4	AAB54927	Anti-HIV								
460	35	100.0	28	4	AAB77375	Core poly								
461	35	100.0	28	4	AAB77227	Core poly								
462	35	100.0	28	4	AAB77372	Core poly								
463	35	100.0	28	4	ABE00231	Viral Dp1								

ALIGNMENTS

RESULT 1

AAR43703

ID AAR43703 standard; peptide; 6 AA.

XX AAR43703;

AC AAR43703;

XX XX

XX XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 10-AUG-1995 (first entry)

XX HIV-1 gp160 epitope, residues 662-667, from isolate BH10.

DE Epitope; gp160; strain; isolate; HIV-1; antibody; monoclonal antibody;

XX 2F5; vaccine.

XX Human immunodeficiency virus 1.

OS EP570357-A2.

XX 18-NOV-1993.

PD 13-MAY-1993; 93EP-00890100.

PF 14-MAY-1992; 92AT-00000997.

PR 29-AUG-1992; 92US-00932787.

XX XX

XX (POLI-) POLIMUN SCI IMMUNBIOLOGISCHE FORSCH GMBH.

PA Katinger H, Rueker F, Himmeler G, Muster T, Purtscher M;

PI Maiwald G, Steindl F, Trkola A;

XX XX

DR WPI; 1993-361543/46.
 DR N-PSDB; AAQ51572.
 XX
 PT Peptides that induce antibodies which neutralise genetically divergent
 PT HIV-1 isolates - used as recombinant fusion proteins, recombinant
 PT chimeric vaccines or recombinant antibodies.
 XX
 PS Claim 1; Page 7; 41pp; English.
 XX
 CC The sequences given in AAQ51572-96 encode epitopes of gp160 derived from
 CC different strains and isolates of HIV-1. The peptides encoded by these
 CC sequences induce antibodies which neutralise genetically divergent HIV-1
 CC isolates. They bind specifically to the monoclonal antibody 2F5. The
 CC peptides comprise just 6 amino acids derived from the gp160 and represent
 CC highly conserved epitopes which means that antibodies raised against them
 CC will be active against a variety of HIV-1 isolates. The peptides can be
 CC used as recombinant fusion proteins, recombinant chimeric vaccines or as
 CC recombinant antibodies. They may also be used to link the variable
 CC domains of a single chain Fv fragment, or to substitute one or more parts
 CC of a MAb peptide sequence. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 2

AAR68698
 ID AAR68698 standard; peptide; 6 AA.

XX AAR68698;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 07-SEP-1995 (first entry)
 XX
 DE Katinger's neutralisation epitope.
 KW T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag;
 KW pol; vaccine; multimeric peptide; AIDS; 3D organisation.
 XX
 OS Human immunodeficiency virus 1.

PN W09429339-A1.
 XX
 PD 22-DEC-1994.
 XX
 PF 08-JUN-1994; 94WO-CA000317.
 XX
 PR 09-JUN-1993; 93US-00073378.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.

XX Sia CDY, Chong P, Klein MH;
 XX WPI; 1995-036400/05.
 DR

XX Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope of
 PT gag protein linked to B-cell epitope of V3 loop protein of an HIV-1
 PT isolate.
 XX

PS Claim 4; Page 16; 69pp; English.

XX This sequence represents a B-cell epitope, which represents the gp41
 CC derived epitope, Katinger's neutralising epitope. This peptide and other

CC peptides containing this sequence may be linked to T-cell epitopes, eg.
 CC T1 or p24E to form a chimeric protein. This chimeric peptide is
 CC recognised by monoclonal antibody 2F5. Chimeric peptides such as this,
 CC may be used in the production of HIV-1 vaccines. These peptide sequences
 CC may also be used in the production of multimeric peptides in which the
 CC peptides are C-terminally modified by the addition of a Lys residue which
 CC is modified on its epsilon amino acid to carry an additional copy of the
 CC peptide molecule. The linear and multimeric peptides may be used for the
 CC treatment of AIDS by acting to displace the binding of HIV virus to human
 CC or animal cells or by disturbing the 3D organisation of the virus.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 3

AAR92010
 ID AAR92010 standard; protein; 6 AA.

XX AAR92010;
 AC
 XX
 DT 16-OCT-2003 (revised)
 DT 27-SEP-1996 (first entry)
 XX
 XX HIV-1 gp41 epitope, for insertion in Mycobacterium alpha antigen.
 XX
 KW Mycobacterium bovis BCG; AIDS vaccine; surface protein; alpha antigen;
 KW Human immunodeficiency virus type 1; fusion protein; gp41 epitope.
 XX
 OS Human immunodeficiency virus 1.

PN W09604009-A1.

XX 15-FEB-1996.

XX 31-JUL-1995; 95WO-JP001515.

XX 29-JUL-1994; 94JP-00178462.

XX (AJIN) AJINOMOTO CO INC.

XX (NINA-) JAPAN AGENCY NAT INST HEALTH.

XX Matsuo K, Chujo Y, Yamazaki A, Honda M, Yamazaki S, Taseaka H;

XX WPI; 1996-129127/13.

XX N-PSDB; AAT16054.

XX BCG containing vaccine secretes chimeric protein containing foreign
 PT antigen - has enhanced immunogenicity and antigenicity esp. when used as
 PT an anti-AIDS vaccine.

XX Example 14; Page 29; 56pp; Japanese.

XX Antigenic peptides can be inserted into the alpha-antigen sequence of a
 CC Mycobacterium and secreted from an appropriately transformed M.bovis BCG
 CC cell. The resulting chimeric antigen has greatly enhanced antigenicity
 CC and immunogenicity and is recognised in vivo by B-cells which recognise
 CC the alpha-antigen. The present sequence is that of a HIV-1 gp41 loop
 CC epitope which was incorporated into the alpha antigen. M.bovis BCG cells
 CC secreting a chimeric protein comprising the epitope sequence are useful
 CC as anti-AIDS vaccines. (Updated on 16-OCT-2003 to standardise OS field)
 XX

SQ Sequence 6 AA;

Thu Mar 18 10:20:33 2004

us-10-024-329-2.rag

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 4
 AAW25868
 ID AAW25868 standard; peptide; 6 AA.
 XX
 AC AAW25868;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-OCT-1997 (first entry)
 XX
 DE HIV-1 gp41 Katanger's neutralisation epitope.
 XX
 KW HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env;
 KW V3 loop; vaccine; determinant; chimaeric.
 XX
 OS Synthetic.
 XX
 PN US5639854-A.
 XX
 PD 17-JUN-1997.
 XX
 PF 09-JUN-1994; 94US-00257528.
 XX
 PR 09-JUN-1993; 93US-00073378.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Klein MH, Sia CDY, Chong P;
 XX
 DR WPI; 1997-332082/30.
 XX
 PT Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag
 PT protein T-cell epitope linked to env protein B-cell epitope.
 XX
 PS Example 1; Col 23-24; 41pp; English.
 XX
 CC The invention relates to new synthetic peptides comprising at least one
 CC amino acid sequence comprising an HIV gag protein T-cell epitope linked
 CC at its C- or N-terminus to an amino acid sequence comprising a B-cell
 CC epitope of the V3 loop of an HIV env protein, which can be used to
 CC generate vaccines against HIV-1. The T-cell epitope sequence is pref.
 CC selected from the T-helper determinant core peptides P24E, P24N, P24L,
 CC P24M and P24H while the B-cell epitopes are derived from HIV strains
 CC including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAI, IIB, RP, 26, 2054,
 CC 1714 and BX08. The peptides are chimaeric and can be linked to a branched
 CC Lys backbone. This is the sequence of the Katanger's neutralisation
 CC epitope from the gp41 protein. The peptide is used in the construction of
 CC the chimaeric T/B cell epitope peptides AAW25853-67. (Updated on 25-MAR-
 CC 2003 to correct PF field.)
 XX
 XX Sequence 6 AA;

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 5
 AAW53143
 ID AAW53143 standard; peptide; 6 AA.
 XX

AC AAW53143;
 XX 20-JUL-1998 (first entry)
 DT
 XX
 DE HIV gp41-contained antibody neutralisation epitope.
 XX
 KW VIJneo; HIV vaccine; codon usage optimisation; HIV; immune response;
 KW human immunodeficiency virus; hepatitis; tuberculosis; tumour;
 KW env protein; gp140 gene; recombinant.
 XX
 OS Human immunodeficiency virus.
 XX
 PN WO9748370-A2.
 XX
 PD 24-DEC-1997.
 XX
 PF 17-JUN-1997; 97WO-US010517.
 XX
 PR 21-JUN-1996; 96US-0020165P.
 PR 21-JUN-1996; 96US-0020166P.
 PR 16-JUL-1996; 96GB-00014942.
 PR 16-JUL-1996; 96GB-00014943.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Shiver JW, Davies ME, Freed DC, Liu MA, Perry HC;
 XX
 DR WPI; 1998-062825/06.
 XX
 PT DNA encoding protein with codon usage optimised for intended host cell -
 PT specifically for DNA vaccines against human immune deficiency virus,
 PT allows rev-independent expression of HIV genes.
 XX
 PS Example 7; Page 39; 113pp; English.
 XX
 CC This is the gp41-contained antibody neutralisation epitope retained in a
 CC HIV gp140 vaccine construct. This is used in a VIJneo expression vector
 CC for vaccine production containing a new synthetic DNA, encoding a protein
 CC or peptide. The synthetic DNA sequence encodes HIV env protein or its
 CC fragment and has codons optimised for expression in a non-homologous
 CC host. The synthetic DNA sequences are used to increase production of
 CC recombinant protein and to induce anti-HIV neutralising antibody, HIV-
 CC specific T-cell immune responses or protective immune responses in
 CC vertebrates, specifically as HIV vaccines. Optimisation of codons results
 CC in increased expression of the DNA in the host. The DNA induces antigen-
 CC presenting cells to stimulate cytotoxic and helper T-cells, and effector
 CC functions such as lymphokine secretion specific to HIV antigens. Cross-
 CC strain protection is achieved without use of adjuvant and the synthetic
 CC DNA may provide a longer-lasting response. The env gene includes a high
 CC proportion of codons rarely used in mammals, so optimisation will allow
 CC this gene to be expressed efficiently in absence of rev. The DNA
 CC sequences, more generally, may express antigens from many other
 CC pathogens, e.g. hepatitis or tuberculosis, and also from tumours
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 6
 AAW67384
 ID AAW67384 standard; peptide; 6 AA.
 XX
 AC AAW67384;
 XX
 DT 25-JAN-1999 (first entry)
 XX

DE katinger's neutralisation epitope.
 XX Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
 KW V3 loop.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX US5817754-A.
 XX
 XX PD 06-OCT-1998.
 XX
 XX PF 05-JUN-1995; 95US-00464329.
 XX
 XX PR 09-JUN-1993; 93US-00073378.
 XX PR 09-JUN-1994; 94US-00257528.
 XX
 XX PA (CONN-) CONNAUGHT LAB LTD.
 XX
 XX PI Chong P, Klein MH, Sia CDY;
 XX WPI; 1998-556461/47.
 XX
 XX DR WPI; 1998-556461/47.
 XX
 XX PT Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell
 PT epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
 XX
 XX PS Disclosure; Col 21-22; 40pp; English.
 XX
 XX CC The invention relates to a novel immunogenic composition for use in
 CC vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
 CC epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
 CC are generally designed based on the p24 core protein and the B-cell
 CC epitopes from the V3 loop of the gp120 protein from various HIV-1
 CC strains. This peptide represents the sequence of the Katinger's
 CC neutralisation epitope and is used to construct the hybrid peptides
 CC AAW67381-W67383
 XX
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELDKWA 6
 Db |||||
 1 ELDKWA 6
 RESULT 7
 AAW99905
 ID AAW99905 standard; peptide; 6 AA.
 XX
 XX AC AAW99905;
 XX
 XX DT 05-MAY-1999 (first entry)
 XX
 XX DE HIV-1 vaccine synthetic peptide SEQ ID NO:69.
 XX
 XX KW HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
 KW gag protein; B-cell epitope; gp41 protein; chimeric; infection.
 XX
 XX OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 XX OS US5876731-A.
 XX
 XX PD 02-MAR-1999.
 XX
 XX PF 05-JUN-1995; 95US-00462507.
 XX
 XX PR 09-JUN-1993; 93US-00073378.
 XX PR 09-JUN-1994; 94US-00257528.
 XX

PA (CONN-) CONNAUGHT LAB LTD.
 XX Chong P, Klein MH, Sia CDY;
 XX WPI; 1999-189590/16.
 XX
 XX PT Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
 PT epitope linked to gp41 B-cell epitope.
 XX
 XX PS Claim 5; Col 72; 41pp; English.
 XX
 XX CC The present invention describes a synthetic peptide comprising an amino
 CC acid sequence containing a T-cell epitope of an HIV gag protein linked at
 CC its C terminus to an amino acid sequence containing a B-cell epitope of
 CC an HIV gp41 protein and containing the amino acid sequence: X1LKDWX2;
 CC where X1 = E, A, G or Q, and X2 = A or T, or an amino acid sequence
 CC capable of eliciting an HIV-specific antiserum and recognizing the
 CC sequence X1LKDWX2. The synthetic peptide is useful in vaccines against
 CC HIV infection and in diagnostic applications. AAW98892 to AAW98906, and
 CC AAW9899 to AAW9989 represent synthetic peptides from the present
 CC invention
 XX
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELDKWA 6
 Db |||||
 1 ELDKWA 6
 RESULT 8
 AAY39717
 ID AAY39717 standard; peptide; 6 AA.
 XX
 XX AC AAY39717;
 XX
 XX DT 17-OCT-2003 (revised)
 XX DT 26-NOV-1999 (first entry)
 XX
 XX DE HIV1 chimeric peptide gp41 epitope.
 XX
 XX KW HIV; vaccine; immunogenic composition; T cell epitope; B cell epitope;
 KW infection; antibody; antiviral.
 XX
 XX OS Human immunodeficiency virus 1.
 XX
 XX OS US5951986-A.
 XX
 XX PD 14-SEP-1999.
 XX
 XX PF 06-JUN-1995; 95US-00467881.
 XX
 XX PR 09-JUN-1993; 93US-00073378.
 XX PR 09-JUN-1994; 94US-00257528.
 XX
 XX PA (CONN-) CONNAUGHT LAB LTD.
 XX
 XX PI Klein MH, Chong P, Sia CDY;
 XX WPI; 1999-550482/46.
 XX
 XX DR Immunogenic composition containing synthetic fusion polypeptides
 XX containing both the T and B cell epitopes of the human immunodeficiency
 XX virus, useful antigens in producing vaccines.
 XX
 XX PS Disclosure; Col 9; 43pp; English.
 XX
 XX CC This sequence represents a fragment of a HIV1 protein, and can be used in
 CC the immunogenic composition of the invention. The composition comprises a
 CC synthetic fusion polypeptide which includes a sequence encoding 1 or more

CC T cell epitopes and a sequence encoding 1 or more B cell epitopes and a
 CC carrier. Both the T cell and B cell epitopes are derived from HIV
 CC proteins. The compositions are useful as vaccines against HIV infection.
 CC The composition induces HIV-1-specific polyclonal antibodies that are
 CC opsonising and antiviral. The peptide components may be selected to
 CC induce a response against different viral isolates and in subjects who
 CC recognise different T cell epitopes. (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0;
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 9
 AAY57748
 ID AAY57748 standard; peptide; 6 AA.
 XX
 AC AAY57748;
 XX
 DT 15-MAR-2000 (first entry)
 XX
 DE Peptide amino acid sequence SEQ ID NO:46.
 XX
 KW Recombinant negative strand viral RNA template; virus particle;
 KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
 KW packaging.
 XX
 OS Unidentified.
 XX
 PN US6001634-A.
 XX
 PD 14-DEC-1999.
 XX
 PF 29-JUN-1998; 98US-00106377.
 XX
 PR 28-AUG-1989; 89US-00399728.
 PR 21-NOV-1989; 89US-00440053.
 PR 22-MAY-1990; 90US-00527237.
 PR 04-AUG-1992; 92US-00925061.
 PR 01-FEB-1994; 94US-00190698.
 PR 01-JUN-1994; 94US-00252508.
 XX
 PA (PALE/) PALESE P.
 PA (GARC/) GARCIA-SASTRE A.
 XX
 PI Palese P, Garcia-Sastre A;
 XX
 DR WPI; 2000-071660/06.
 XX
 PT Chimeric virus containing influenza virus RNA segments, useful for
 PT expressing heterologous gene products in appropriate host cell systems.
 XX
 PS Disclosure; Col 73; 67pp; English.
 XX
 CC The present invention describes a chimeric virus comprising influenza
 CC virus containing a heterologous RNA segment from another strain of
 CC influenza virus or 8 genomic segments from different strains of influenza
 CC virus, with each segment comprising the reverse complement of a mRNA
 CC coding sequence operatively linked to a binding site specific for an RNA-
 CC directed RNA polymerase of a negative strand RNA virus. The recombinant
 CC negative strand virus RNA templates may be used to express heterologous
 CC gene products in appropriate host cell systems and/or to construct
 CC recombinant viruses that express, package and/or present the heterologous
 CC gene product. The expression products and chimeric viruses may be used in
 CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
 CC represent sequences used in the exemplification of the present invention

XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 35; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0;
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 10
 AAB24104
 ID AAB24104 standard; peptide; 6 AA.
 XX
 AC AAB24104;
 XX
 DT 12-SEP-2003 (revised)
 DT 29-JAN-2001 (first entry)
 XX
 DE HIV-1 gp41 epitope recognised by human MAb 2F5 SEQ ID NO:1.
 XX
 KW HIV-1; human immunodeficiency virus; human; epitope; gp41; MAb;
 KW monoclonal antibody; antiviral; antiHIV; infection; inhibition;
 KW replication.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200055377-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 15-MAR-2000; 2000WO-US006771.
 XX
 PR 17-MAR-1999; 99US-0124907P.
 PR 14-MAR-2000; 2000US-00525874.
 XX
 PA (NYBL-) NEW YORK BLOOD CENT INC.
 PA (JIAN/) JIANG S.
 PA (DEBN/) DEBNATH A K.
 XX
 PI Jiang S, Debnath AK;
 XX
 DR WPI; 2000-656011/63.
 XX
 PT Screening assay for antiviral compounds targeted to HIV-1 gp41 core
 PT structure involves utilizing conformation-specific monoclonal antibody,
 PT which is reactive with fusion active gp41 of the virus.
 XX
 PS Example 1c; Page 29; 79pp; English.
 XX
 CC The present invention describes a method for screening (M1) an antiviral
 CC compound (AC) targeted to the HIV-1 gp41 core structure. The method
 CC involves capturing polyclonal antibodies (PAB) directed against trimer of
 CC heterodimer (A) which contains N- and C-peptide (NP,Cp) onto a solid-
 CC phase, to form a PAB-coated solid-phase that is added with mixture of NP,
 CC CP, and AC, adding monoclonal antibody (MAb) directed against (A) and
 CC measuring the binding of MAb. The antivirals identified by the method are
 CC useful for inhibiting HIV-1 replication or infectivity in cells, in
 CC patients and for treating the patients infected with HIV-1. The method
 CC distinguishes the anti-HIV-1 agents targeting the gp41 core domain from
 CC those having different targets. Since the residues located at the
 CC interaction sites in both the N-terminal heptad repeat (NHR) and C-
 CC terminal heptad repeat (CHR) regions of gp41 are highly conserved, the
 CC antiviral agents targeted to the gp41 core are considered to have broader
 CC specificity against infection by HIV strains than those targeted to
 CC gp120. The present sequence represents an HIV-1 gp41 epitope used in an
 CC example from the present invention, which is recognised by the human MAb
 CC 2F5. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 11

AAG63933
ID AAG63933 standard; peptide; 6 AA.

XX AC AAG63933;

XX DT 11-SEP-2003 (revised)

XX DT 29-OCT-2001 (first entry)

XX DE Amino acid sequence of a HIV-1 gp41 peptide fragment.

XX KW HIV-1; gp41; viral entry; envelope protein; glycoprotein;
viral infection; antiviral.

XX OS Human immunodeficiency virus 1.

XX PN WO200159457-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004030.

XX PR 10-FEB-2000; 2000US-0181543P.

XX PR 28-SEP-2000; 2000US-0235901P.

XX PA (PANA-) PANACOS PHARM INC.

XX PI Wild CT, Allaway GP;

XX DR WPI; 2001-522493/57.

XX PT Screening for inhibitors of viral entry structure formation by
selectively triggering the formation of one or more critical entry
PT intermediates in cell-surface-expressed viral envelope and probing for
PT its formation.

XX PS Disclosure; Page 37; 68pp; English.

XX CC The present sequence represents a fragment of a Human immunodeficiency
virus type 1 (HIV-1) gp41 protein. The peptide is used to raise
CC antibodies for use in the method of the invention. The specification
CC describes a method of screening for inhibitors of viral entry structure
CC formation. The method comprises contacting a viral envelope protein or
CC glycoprotein (e.g. gp41) with a triggering agent and a candidate compound
CC to form a mixture, and measuring the effect that the candidate compound
CC has on the formation of conformational intermediates. The effect of the
CC candidate compound can be measured by antibody binding to these
CC conformational intermediates. The compounds identified by the method are
CC useful as inhibitors for inhibiting or preventing viral infection and to
CC treat humans infected with HIV-1 or other viruses. This antiviral
CC compounds can also be used to inactivate viruses in body fluids, e.g.
CC blood or blood compounds used for therapeutic purposes. The assay is also
CC useful for detecting antibodies in virus-infected individuals or virus-
CC infected body fluids or tissues that inhibit entry-relevant
CC conformational changes in one or more viral envelope proteins or
CC glycoproteins. The presence of the antibodies in infected individuals or
CC samples is of prognostic value. (Updated on 11-SEP-2003 to standardise OS
CC field)

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 12

AAB92333
ID AAB92333 standard; peptide; 6 AA.

XX AC AAB92333;

XX DT 22-JUN-2001 (first entry)

XX DE Virus related peptide SEQ ID NO:1509.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US013576.

XX PR 17-MAY-1999; 99US-0134406P.

XX PR 10-SEP-1999; 99US-0153406P.

XX PR 15-OCT-1999; 99US-0159783P.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
peptidase degradation, useful for increasing length of in vivo activity.

XX PS Disclosure; Page 699; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)
comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 13
AAG65282
ID AAG65282 standard; peptide; 6 AA.
XX AC
XX AC
XX AC
XX AC
DT 11-SEP-2003 (revised)
DT 30-NOV-2001 (first entry)
XX HIV-1 isolate BH10 gp41 protein fragment (residues 662-667).
DE HIV-1; gp120; BH10; vaccine; immunization; gp41 protein.
XX HIV-1; gp120; BH10; vaccine; immunization; gp41 protein.
OS Human immunodeficiency virus 1.
XX US6268484-B1.
FN 31-JUL-2001.
PD 30-JUL-1998; 98US-00124900.
XX 19-APR-1995; 95WO-EP001481.
PR 07-JUN-1995; 95US-00478536.
XX (POLY-) POLYMER SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX Katinger H, Buchacher A, Ernst W, Ballaun C, Purtscher M;
PI Trkola A, Predl R, Schmatz C, Klima A, Steindl F, Muster T;
XX WPI; 2001-556601/62.
XX New anti-idiotypic antibodies consisting of one or both amino acid
PT sequences corresponding to amino acid positions 79-84 or 325-400 of the
PT processed gp120 of HIV-isolate BH10, useful as vaccine against HIV-1
PT infections.
XX Disclosure; Col 1; 27pp; English.
XX The invention relates to a peptide fragment comprising of amino acid
CC sequences corresponding to sequences within the processed gp120 of HIV-1
CC isolate BH10 (GenBank accession M15654). The peptides are useful in the
CC detection, prevention and treatment of HIV-1 infections, and in AIDS
CC therapy. The antibodies are especially useful as vaccines for active and
CC passive immunization, or for the detection and/or determination of HIV-1
CC infected cells and/or HIV-1 viruses. The present sequence represents the
CC HIV-1 isolate BH10 gp41 peptide fragment. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX SQ
Sequence 6 AA;
Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 ELDKWA 6
DB 1 ELDKWA 6
RESULT 14
AAB98918
ID AAB98918 standard; peptide; 6 AA.
XX AC
XX AC
XX AC
DT 25-SEP-2001 (first entry)
XX HIV epitope ELDKWA.
XX HIV-specific immunogen; major histocompatibility complex; MHC class I;
KW MHC class II; antigen presentation; CD8+ response; CD4+ response;
KW gene therapy; genetic vaccine; anti-HIV; antiviral; antiretroviral;
KW epitope.

XX OS
XX Human immunodeficiency virus.
XX WO200154701-A1.
XX PD
XX 02-AUG-2001.
XX 26-JAN-2001; 2001WO-US002766.
XX 31-JAN-2000; 2000US-0179276P.
XX (AVET) AVENTIS PASTEUR SA.
XX (AARO-) AARON DIAMOND AIDS RES CENT.
XX Ho D, Markowitz M, Klein M, El Habib R;
XX WPI; 2001-488741/53.
XX Permitting cessation of antiviral therapy on HIV-infected patients
PT undergoing antiviral therapy, useful for treating HIV-infected patients,
PT by administering nucleic acid based vaccines encoding HIV-specific
PT immunogens.
XX Claim 29; Page 41; 57pp; English.
XX The invention relates to a method for permitting the cessation of
CC antiviral therapy in HIV-infected patients undergoing antiviral therapy
CC who have a controlled level of viraemia. The method involves
CC administration of nucleic-acid based vaccines encoding HIV-specific
CC immunogens to the patient's cells, enabling the expression of the HIV-specific
CC immunogens in the patient's cells. The HIV-specific antigens are
CC presented on major histocompatibility complex (MHC) class I and II
CC molecules, stimulating an HIV-specific CD8+ and CD4+ response. The method
CC permits the cessation of antiviral therapy on HIV-infected patients
CC either without virus rebound, with a delayed rebound, or with decreased
CC post-rebound set point, in addition to achieving immunological control of
CC persistent infectious virus after discontinuation of antiviral therapy.
CC The method is useful for people who have lost their CD4+ and/or CD8+ T
CC cell responses to HIV antigens, such as those who have lost their
CC proliferative T cell responses to gp120 or p24. The method is
CC specifically useful for treating persons infected with a lymphotropic or
CC immune-destroying retroviral infection, or for treating HIV-infected
CC patients undergoing anti-retroviral therapy and having a viral load of
CC less than 10000, preferably 1000 viral copies/ml of plasma and a CD4+
CC cell count of above 300 cells/ml, preferably 500 cells/ml. The present
CC sequence represents an HIV epitope which may be encoded by a genetic
CC vaccine of the invention
XX SQ
Sequence 6 AA;
Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 ELDKWA 6
DB 1 ELDKWA 6
RESULT 15
AAG63974
ID AAG63974 standard; peptide; 6 AA.
XX AC
XX AC
XX AC
DT 11-SEP-2003 (revised)
DT 13-NOV-2001 (first entry)
XX Amino acid sequence of a HIV-1 gp41 derived peptide.
XX Nonstructural gene; NS gene; influenza A virus; NS1 gene; vaccine;
KW viral infection; influenza infection; HIV-1 infection; gp41.
XX

OS Human immunodeficiency virus 1.
 PN WO200164860-A2.
 XX
 PD 07-SEP-2001.
 XX
 XX 02-MAR-2001; 2001WO-EP002392.
 PF
 XX 02-MAR-2000; 2000EP-00104338.
 PR
 XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
 PA
 XX Ferko B, Egorov A, Voglauer R;
 PI
 XX WPI; 2001-514840/56.
 DR
 XX Recombinant NS gene of an influenza A virus comprising a functional RNA
 PT binding domain and a gene sequence modification after nucleotide position
 PT 400 of the NS1 gene segment, useful for producing a live attenuated
 PT influenza virus vaccine.
 XX
 XX Claim 3; Page 25; 40pp; English.
 PS
 XX The specification describes a recombinant nonstructural (NS) gene of an
 CC influenza A virus. The gene comprises a functional RNA binding domain and
 CC a gene sequence modification after nucleotide position 400 of the NS1
 CC gene segment, counted on the basis of influenza A/PR/8/34 virus, where
 CC the modification bars transcription of the remaining portion of the NS1
 CC gene segment. The recombinant NS gene is used to produce a vaccine, which
 CC is useful for prophylactic or therapeutic application against a viral
 CC infection, preferably against influenza or HIV-1 infection. Influenza
 CC virus transfectants that contain the modified NS gene may have an
 CC interferon (IFN) inducing phenotype, but may or may not be sensitive
 CC towards IFN. The present sequence represents a gp41 epitope, and was
 CC used to modify the NS genes of the invention. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6
 RESULT 16
 ABB07403
 ID ABB07403 standard; peptide; 6 AA.
 XX
 AC ABB07403;
 XX
 DT 29-AUG-2003 (revised)
 DT 09-APR-2002 (first entry)
 XX
 XX HIV-1 gp41 epitope fragment.
 DE
 XX Coat protein; potyvirus; bean yellow mosaic virus; BYMV; immunogenic;
 KW plant virion; vaccine; NDV; Newcastle Disease virus; HIV; gp41; PVX; PVY;
 KW potato virus; epitope.
 KW
 XX Human immunodeficiency virus 1.
 OS
 XX WO200200169-A2.
 PN
 XX 03-JAN-2002.
 PD
 XX 26-JUN-2001; 2001WO-US020272.
 PF
 XX 26-JUN-2000; 2000US-00603997.
 PR
 XX
 XX

PA (USDA) US DEPT OF AGRICULTURE.
 XX
 XX Hammond R, Zhao Y, Hammond J;
 XX
 DR WPI; 2002-139854/18.
 XX
 XX New cDNA constructs comprising a bean yellow mosaic virus (BYMV) DNA
 PT sequence or a DNA sequence encoding a fusion coat protein, useful for
 PT generating quantities of immunogenic peptides for vaccine and antibody
 PT production.
 XX
 XX Claim 5; Page 26; 52pp; English.
 PS
 XX The invention provides a cDNA construct, containing a DNA sequence that
 CC encodes a fusion coat protein comprising a truncated potyvirus coat
 CC protein and a foreign antigenic peptide. The cDNA construct comprises a
 CC bean yellow mosaic virus (BYMV) DNA. The cDNA constructs and vectors are
 CC useful for generating the expressed immunogenic peptides. The cDNA
 CC constructs and vectors are useful for systemically infecting a plant to
 CC produce stable recombinant plant virions expressing foreign peptides, as
 CC a means of producing and purifying large amounts of foreign peptides to
 CC be used as genetically engineered vaccines or for antibody production.
 CC These are particularly useful for producing and purifying large amounts
 CC of NDV (newcastle disease virus) vaccine. A method of producing a foreign
 CC antigenic peptide in a plant comprises infecting a host plant with PVY
 CC (potato virus Y) virions, inoculating the PVY-infected host plant with
 CC the infectious RNA, culturing the plant under conditions to foster plant
 CC growth and transencapsidation; and recovering the transencapsidated PVY
 CC virions from the leaves of the plant. The PVY virions contain foreign
 CC antigenic peptide inserts on the exposed surface of the coat protein of
 CC the virion, the inserts resulting from a transencapsidation process
 CC during virion assembly where copies of PVX (potato virus X) coat protein
 CC containing the fusion coat protein and copies of PVY coat protein
 CC assemble to form the PVY capsid. The present sequence represents HIV-1
 CC gp41 epitope fragment. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 35; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6
 RESULT 17
 AAO14868
 ID AAO14868 standard; peptide; 6 AA.
 XX
 AC AAO14868;
 XX
 DT 19-JUL-2002 (first entry)
 DT
 XX HIV epitope peptide 2.
 DS
 XX HIV, acquired immunodeficiency syndrome; AIDS; vaccine;
 KW HIV neutralising epitope; CTL epitope.
 KW
 XX Human immunodeficiency virus.
 OS
 XX WO200226253-A1.
 PN
 XX 04-APR-2002.
 PD
 XX 20-JUL-2001; 2001WO-CN001190.
 XX
 PF
 XX 18-AUG-2000; 2000CN-00123487.
 PR
 XX (UYOI) UNIV QINGHUA.
 PA (JIAN-) JIANGXI DRAGON FLY SCI & TECHNOLOGY CO LT.
 PA (BEIJ-) BEIJING GUOXIWEIYE HIGH TECHNOLOGY DEV C.

XX	Chen Y, Ding J, Lu Y, Chen Y;	XX	Chen Y, Ding J, Lu Y, Chen Y;
XX	WPI; 2002-372090/40.	XX	WPI; 2002-372090/40.
XX	Vaccines for acquired immunodeficiency syndrome comprises epitope	XX	Vaccines for acquired immunodeficiency syndrome comprises epitope
PT	polypeptides as conjugates with carrier protein or polypeptide.	PT	polypeptides as conjugates with carrier protein or polypeptide.
XX	Claim 3; Page 6; 12pp; Chinese.	XX	Claim 3; Page 6; 12pp; Chinese.
XX	The invention comprises an acquired immunodeficiency syndrome (AIDS)	XX	The invention comprises an acquired immunodeficiency syndrome (AIDS)
CC	vaccine. The AIDS vaccine contains at least one human immunodeficiency	CC	vaccine. The AIDS vaccine contains at least one human immunodeficiency
CC	virus (HIV) neutralising epitope peptide or a cytotoxic T lymphocyte	CC	virus (HIV) neutralising epitope peptide or a cytotoxic T lymphocyte
CC	(CTL) epitope conjugated to a carrier protein. The vaccines of the	CC	(CTL) epitope conjugated to a carrier protein. The vaccines of the
CC	invention are useful for treating AIDS. Amino acid sequences AAO14865 -	CC	invention are useful for treating AIDS. Amino acid sequences AAO14865 -
CC	AAO14898 represent HIV epitope peptides of the invention	CC	AAO14898 represent HIV epitope peptides of the invention
XX	Sequence 6 AA;	XX	Sequence 6 AA;
XX	Query Match 100.0%; Score 35; DB 5; Length 6;	XX	Query Match 100.0%; Score 35; DB 5; Length 6;
XX	Best Local Similarity 100.0%; Pred. No. 1.4e+06;	XX	Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ELDKWA 6	QY	1 ELDKWA 6
DB		DB	
XX	1 ELDKWA 6	XX	1 ELDKWA 6
XX	ABR62944	XX	ABR62944
XX	ABR62944 standard; peptide; 6 AA.	XX	ABR62944 standard; peptide; 6 AA.
XX	04-DEC-2003 (first entry)	XX	04-DEC-2003 (first entry)
XX	HIV-1 virus envelope ectodomain gp41 core epitope.	XX	HIV-1 virus envelope ectodomain gp41 core epitope.
XX	HIV-1; anti-idiotypic; antibody; anti-HIV; virucide; vaccine.	XX	HIV-1; anti-idiotypic; antibody; anti-HIV; virucide; vaccine.
XX	Human immunodeficiency virus type 1.	XX	Human immunodeficiency virus type 1.
XX	WO2003059953-A2.	XX	WO2003059953-A2.
XX	24-JUL-2003.	XX	24-JUL-2003.
XX	17-JAN-2003; 2003WO-EP000455.	XX	17-JAN-2003; 2003WO-EP000455.
XX	17-JAN-2002; 2002EP-00001250.	XX	17-JAN-2002; 2002EP-00001250.
XX	(POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.	XX	(POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX	Kunert R, Weik R, Stiegler G, Katinger H;	XX	Kunert R, Weik R, Stiegler G, Katinger H;
XX	WPI; 2003-598509/56.	XX	WPI; 2003-598509/56.
XX	New anti-idiotypic antibody inducing HIV-1 neutralizing antibodies,	XX	New anti-idiotypic antibody inducing HIV-1 neutralizing antibodies,
XX	useful as a screening tool or diagnostic agent, and for the manufacture	XX	useful as a screening tool or diagnostic agent, and for the manufacture
XX	of a vaccine, for prophylactic or therapeutic application against HIV-1	XX	of a vaccine, for prophylactic or therapeutic application against HIV-1
XX	infection.	XX	infection.
XX	Claim 2; Page 25; 32pp; English.	XX	Claim 2; Page 25; 32pp; English.
XX	The present sequence is that of a highly conserved epitope sequence on	XX	The present sequence is that of a highly conserved epitope sequence on
XX	the HIV-1 envelope ectodomain gp41. The invention provides an antibody,	XX	the HIV-1 envelope ectodomain gp41. The invention provides an antibody,
XX	or its fragment, which is reactive with HIV-1 neutralising antibody 2F5	XX	or its fragment, which is reactive with HIV-1 neutralising antibody 2F5
XX	(ECACC 90091704) and which inhibits or prevents the HIV-1 neutralisation	XX	(ECACC 90091704) and which inhibits or prevents the HIV-1 neutralisation
XX	activity of 2F5 and/or the binding of 2F5 to HIV-1 gp41. The antibody	XX	activity of 2F5 and/or the binding of 2F5 to HIV-1 gp41. The antibody
XX	preferably inhibits or prevents the binding of 2F5 to proteins or	XX	preferably inhibits or prevents the binding of 2F5 to proteins or
XX	peptides that comprise the HIV-1 gp41 conserved epitope or its variants	XX	peptides that comprise the HIV-1 gp41 conserved epitope or its variants
XX	(see ABR62945-55). Upon administration to a mammal, the antibody elicits	XX	(see ABR62945-55). Upon administration to a mammal, the antibody elicits
XX	Ab3-type antibodies that have HIV-1 neutralising activity and/or that	XX	Ab3-type antibodies that have HIV-1 neutralising activity and/or that
XX	complete with 2F5 for binding to proteins comprising the conserved epitope	XX	complete with 2F5 for binding to proteins comprising the conserved epitope
XX	or its variants. The antibody is preferably an Ab2-type antibody which is	XX	or its variants. The antibody is preferably an Ab2-type antibody which is
XX	anti-idiotypic to 2F5, is monoclonal and is produced by hybridoma cell	XX	anti-idiotypic to 2F5, is monoclonal and is produced by hybridoma cell
XX	line 306 (ECACC 01100279), or is a chimeric or humanized antibody. The	XX	line 306 (ECACC 01100279), or is a chimeric or humanized antibody. The
XX	antibody or its fragment may be coupled, linked or fused to an	XX	antibody or its fragment may be coupled, linked or fused to an
XX	immunoreactive molecule, such as interleukin-4 or interleukin-15, that	XX	immunoreactive molecule, such as interleukin-4 or interleukin-15, that
XX	increases or intensifies a B cell response. It can be used as a screening	XX	increases or intensifies a B cell response. It can be used as a screening
XX	tool, diagnostic or therapeutic agent, or as a vaccine against HIV-1	XX	tool, diagnostic or therapeutic agent, or as a vaccine against HIV-1
XX	infection	XX	infection
XX	Sequence 6 AA;	XX	Sequence 6 AA;
XX	Query Match 100.0%; Score 35; DB 7; Length 6;	XX	Query Match 100.0%; Score 35; DB 7; Length 6;
XX	Best Local Similarity 100.0%; Pred. No. 1.4e+06;	XX	Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ELDKWA 6	QY	1 ELDKWA 6
DB		DB	
XX	1 ELDKWA 6	XX	1 ELDKWA 6
XX	ABR39670	XX	ABR39670
XX	ABR39670 standard; peptide; 6 AA.	XX	ABR39670 standard; peptide; 6 AA.
XX	23-OCT-2003 (revised)	XX	23-OCT-2003 (revised)
XX	23-JUN-2003 (first entry)	XX	23-JUN-2003 (first entry)
XX	HIV-1 gp41 peptide fragment.	XX	HIV-1 gp41 peptide fragment.
XX	HIV-1; immune response; gp41; anti-HIV; vaccine; mAb 4E10-IgG1;	XX	HIV-1; immune response; gp41; anti-HIV; vaccine; mAb 4E10-IgG1;
XX	anti-idiotypic antibody.	XX	anti-idiotypic antibody.
XX	Human immunodeficiency virus 1.	XX	Human immunodeficiency virus 1.
XX	WO2003022879-A2.	XX	WO2003022879-A2.
XX	20-MAR-2003.	XX	20-MAR-2003.
XX	09-SEP-2002; 2002WO-EP010070.		

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 20
ADC79307
ID ADC79307 standard; peptide; 6 AA.
XX
AC ADC79307;
DT 01-JAN-2004 (first entry)
XX
DE HIV-1 gp41 peptide SEQ ID NO:2.
XX
KW immune response; anti-HIV; vaccine; HIV infection.
XX
OS Human immunodeficiency virus 1.
XX
PN WO2003075849-A2.
XX
PD 18-SEP-2003.
XX
PF 06-MAR-2003; 2003WO-US007073.
XX
PR 06-MAR-2002; 2002US-0362247P.
XX
PA (UYAR-) UNIV ARIZONA.
XX
PI Mor TS, Matoba N, Arntzen CJ;
XX
DR WPI; 2003-779033/73.
XX
PT New composition comprising a peptide and a cholera toxin, useful for
PT enhancing immune response in an animal against HIV infection.
XX
PS Claim 1; SEQ ID NO 2; 33pp; English.
XX
CC The present invention describes a composition (C) for enhancing the
CC immune response in an animal. (C) comprises a peptide selected from the
CC group ADC79306, ADC79307, ADC79308, ADC79309, ADC79310, ADC79311 and
CC ADC79312. Also described: (1) enhancing the immune response in an animal;
CC (2) delivering a cargo protein to an animal cell; (3) genetically-
CC modified living cell capable of enhancing immune response in an animal
CC comprising a first DNA sequence encoding a peptide; and (4) constructing
CC a fusion protein for enhancing immune response in an animal. (C) has anti-
CC -HIV activities, and can be used in vaccines. The composition (C) can be
CC used for enhancing the immune response in an animal against HIV
CC infection.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 21
AAR71631
ID AAR71631 standard; peptide; 7 AA.
XX
AC AAR71631;
DT 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
XX
DE HIV-1 gp41 peptide.
XX
KW HIV-1; gp41; gp160; 2FS epitope; antibody; cell fusion; AIDS; vaccine;

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 22
AAR94444
ID AAR94444 standard; peptide; 7 AA.
XX
AC AAR94444;
XX
DT 16-OCT-2003 (revised)
DT 31-MAY-1996 (first entry)
XX
DE HIV-1 gp41 B-cell and neutralising epitope.
XX
KW Molecular presentation; FHV; virion-like particle; capsid protein;
KW capsomer; RNA-2 gene; epitope; HIV-1; vaccine.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9605293-A1.
XX
PD 22-FEB-1996.
XX
PF 04-AUG-1995; 95WO-EP003114.
XX
PR 08-AUG-1994; 94AT-00001545.
XX
PA (UNNA-) UNITED NATIONS IND DEV ORG.
XX
PI Baralle FE, Scodeller E, Tisminetzky S;
XX
DR WPI; 1996-139691/14.
XX
PT New molecular presentation system - comprising a viral protein from a

immunogen; therapy; human immunodeficiency virus type 1;
monoclonal antibody; MAb.
Synthetic.
WO9507354-A1.
16-MAR-1995.
12-SEP-1994; 94WO-EP003039.
11-SEP-1993; 93EP-00114631.
(POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
Katinger H, Muster T;
WPI; 1995-123428/16.
New peptide(s) corresponding to a HIV-1 gp 160 epitope - used to elicit
antibodies which neutralise different HIV-1 strains and inhibit cell
fusion caused by HIV-1.
Claim 1; Page 17; 28pp; English.
The peptides given in AAR71631-36 are based on amino acids 661-668 of HIV
-1 isolate BH10 gp41, the epitope of human MAB 2F5. The peptides may be
inserted into antigenic sites of a viral protein, e.g. influenza virus
hemagglutinin, by gene fusion, for HIV-1 vaccine development. (Updated on
25-MAR-2003 to correct PN field.)
Sequence 7 AA;

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us-10-024-329-2.rag

```

PT small insect virus in which heterologous amino acid sequences are
PT inserted.
XX
XX Disclosure; Page 7; 39pp; English.
XX
XX An HIV-1 gp41 B-cell and neutralising epitope (AAR94444) may be inserted
CC into the outward-directed L1, L2, L3, L4 or L5 loop of the Flock House
CC virus capsid protein (AAR88755). The capsid protein provides a
CC conformationally suitable location for this (or other, see AAR94430-43
CC and AAR94445) heterologous peptides. A molecular presentation system is
CC obd. The FHV recombinant capsomer can be expressed in E. coli.
CC Alternatively, expression in insect cells using a baculovirus vector
CC results in prodn. of mature virus-like particles. (Updated on 16-OCT-2003
CC to standardise OS field)
XX
XX Sequence 7 AA;
SQ
    Query Match      100.0%; Score 35; DB 2; Length 7;
    Best Local Similarity 100.0%; Pred. No. 1.4e+06;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 ELDKWA 6
    Db 1 ELDKWA 6
    RESULT 24
    ID AAW67413 standard; peptide; 7 AA.
    XX
    XX AAW67413;
    DT 25-JAN-1999 (first entry)
    XX
    DE HIV-1 gp41 protein neutralisation epitope.
    XX
    KW Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
    KW V3 loop.
    XX
    OS Synthetic.
    OS Human immunodeficiency virus 1.
    XX
    PN US5817754-A.
    XX
    PD 06-OCT-1998.
    PF 05-JUN-1995; 95US-00464329.
    XX
    PR 09-JUN-1993; 93US-00073378.
    PR 09-JUN-1994; 94US-00257528.
    XX
    PA (CONN-) CONNAUGHT LAB LTD.
    XX
    PI Chong P, Klein MH, Sia CDY;
    XX WPI; 1998-556461/47.
    XX
    PT Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell
    PT epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
    XX
    PS Disclosure; Col 9; 40pp; English.
    XX
    CC The invention relates to a novel immunogenic composition for use in
    CC vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
    CC epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
    CC are generally designed based on the p24 core protein and the B-cell
    CC epitopes from the V3 loop of the gp120 protein from various HIV-1
    CC strains. This sequence corresponds to the neutralisation epitope from the
    CC HIV-1 protein gp41
    XX
    SQ Sequence 7 AA;
    Query Match      100.0%; Score 35; DB 2; Length 7;
    Best Local Similarity 100.0%; Pred. No. 1.4e+06;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 ELDKWA 6
    Db 1 ELDKWA 6
    RESULT 25
    ID AAW99911 standard; peptide; 7 AA.
    XX
    XX AAW99911;
    CC

```

XX 05-MAY-1999 (first entry)
 XX HIV-1 vaccine synthetic peptide SEQ ID NO:98.
 XX
 DE
 XX
 XX HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
 KW gag protein; B-cell epitope; gp41 protein; chimeric; infection.
 XX
 XX Synthetic.
 OS Human immunodeficiency virus 1.
 OS
 XX
 XX US5876731-A.
 PN
 XX
 XX 02-MAR-1999.
 PD
 XX
 XX 05-JUN-1995; 95US-00462507.
 PP
 XX
 XX 09-JUN-1993; 93US-00073378.
 PR
 XX 09-JUN-1994; 94US-00257528.
 XX
 XX (CONN-) CONNAUGHT LAB LTD.
 PA
 XX Chong P, Klein MH, Sia CDY;
 PI WPI; 1999-189590/16.
 XX
 XX Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
 PT epitope linked to gp41 B-cell epitope.
 PT
 XX
 XX Claim 7; Col 72; 41pp; English.
 PS
 XX The present invention describes a synthetic peptide comprising an amino
 CC acid sequence containing a T-cell epitope of an HIV gag protein linked at
 CC its C terminus to an amino acid sequence containing a B-cell epitope of
 CC an HIV gp41 protein and containing the amino acid sequence: X1LKDWX2;
 CC where X1 = E, A, G or Q, and X2 = A or T, or an amino acid sequence
 CC capable of eliciting an HIV-specific antiserum and recognizing the
 CC sequence X1LKDWX2. The synthetic peptide is useful in vaccines against
 CC HIV infection and in diagnostic applications. AAW98892 to AAW98906, and
 CC AAW98899 to AAW99989 represent synthetic peptides from the present
 CC invention
 CC
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 35; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 DB |||||
 1 ELDKWA 6
 RESULT 26
 ID AAY39741 standard; peptide; 7 AA.
 XX
 XX AAY39741;
 AC
 XX
 XX 17-OCT-2003 (revised)
 DT 26-NOV-1999 (first entry)
 XX
 XX HIV1 chimeric peptide gp41.
 DE
 XX
 XX HIV; vaccine; immunogenic composition; T cell epitope; B cell epitope;
 KW infection; antibody; antiviral.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX US5951986-A.
 PN
 XX 14-SEP-1999.
 PD
 XX

PF 06-JUN-1995; 95US-00467881.
 XX
 XX 09-JUN-1993; 93US-00073378.
 PR 09-JUN-1994; 94US-00257528.
 XX
 XX (CONN-) CONNAUGHT LAB LTD.
 PA
 XX Klein MH, Chong P, Sia CDY;
 PI WPI; 1999-550482/46.
 DR
 XX
 XX Immunogenic composition containing synthetic fusion polypeptides
 PT containing both the T and B cell epitopes of the human immunodeficiency
 PT virus, useful antigens in producing vaccines.
 XX
 XX Disclosure; Col 9; 43pp; English.
 PS
 XX This sequence represents a fragment of a HIV1 protein, and can be used in
 CC the immunogenic composition of the invention. The composition comprises a
 CC synthetic fusion polypeptide which includes a sequence encoding 1 or more
 CC T cell epitopes and a sequence encoding 1 or more B cell epitopes and a
 CC carrier. Both the T cell and B cell epitopes are derived from HIV
 CC proteins. The compositions are useful as vaccines against HIV infection.
 CC The composition induces HIV-1-specific polyclonal antibodies that are
 CC opsonising and antiviral. The peptide components may be selected to
 CC induce a response against different viral isolates and in subjects who
 CC recognise different T cell epitopes. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 CC
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 35; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 DB |||||
 1 ELDKWA 6
 RESULT 27
 ID AAB29401 standard; peptide; 7 AA.
 XX
 XX AAB29401;
 AC
 XX 12-SEP-2003 (revised)
 DT 09-FEB-2001 (first entry)
 XX
 XX HIV-1 envelope protein gp41 epitope, SEQ ID NO:1.
 DE
 XX
 XX HIV-1 gp41; epitope; conserved peptide; monoclonal antibody; Mab 2F5;
 KW Fab' fragment; protein co-ordinate data; crystal structure;
 KW X-ray crystallography; three-dimensional structure;
 KW epitope analogue design; immunogenic; anti-HIV vaccine.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX WO2000061618-A1.
 EN
 XX 19-OCT-2000.
 PD
 XX
 XX 05-APR-2000; 2000WO-CA000358.
 PF
 XX
 XX 13-APR-1999; 99US-00289942.
 PR
 XX (UTOR) UNIV TORONTO.
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 XX
 XX Pai EF, Klein MH, Chong P, Pedyczak A;
 XX WPI; 2000-679465/66.
 DR
 XX

PT Three dimensional structure of Fab' fragment of human immunodeficiency
PT virus-1 cross-neutralizing monoclonal antibody 2F5, complexed or
PT uncomplexed with a peptide for construction of peptide analogs and
PT peptide mimetics.

XX Claim 13; Page 30; 42pp; English.

XX The invention relates to an isolated crystal of the Fab' fragment of
CC monoclonal antibody (Mab) 2F5. Mab 2F5 binds an epitope (AAB29401) of the
CC HIV-1 envelope protein gp41. The Mab 2F5 Fab' fragment may be complexed
CC or uncomplexed with the gp41 epitope (or a functional analogue thereof) in
CC the crystal of the invention. Elucidation of the three- dimensional
CC structures of 2F5 Fab' in the epitope-complexed and uncomplexed states
CC enables construction of peptide mimetics constrained in the same complex,
CC turn-like configuration as seen in the crystal structure of the complex,
CC providing an increased immunogenicity to the epitope sequence.

CC Elucidation of the crystal structure of Fab' 2F5 when bound to the
CC peptide GluLeuAspLysTrpSer provides details of the actual conformation of
CC the peptide epitope when it is bound to the antibody. The conformation of
CC the peptide epitope provides the basis for the provision of peptide
CC analogs, peptide mimetics and other antigens which are useful as
CC components of an anti-HIV vaccine. The present sequence represents the
CC HIV-1 gp41 epitope which binds to Mab 2F5. (Updated on 12-SEP-2003 to
CC standardise OS field)

XX Sequence 7 AA;

Query Match 100.0%; Score 35; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 28
AAU70190
ID AAU70190 standard; peptide; 7 AA.
XX AAU70190;
XX 14-FEB-2002 (first entry)
XX P3 peptide linear binding region.
XX Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
KW alpha-helical region, ectodomain.
XX Homo sapiens.
XX WO200170262-A2.
XX 27-SEP-2001.
XX 15-MAR-2001; 2001WO-US008108.
XX 17-MAR-2000; 2000US-0189981P.
XX (PANA-) PANACOS PHARM INC.
XX Wild CT, Allaway GP;
XX WPI; 2001-626098/72.
XX Immunogenic composition for inhibiting HIV infection, comprises viral
PT envelope protein or its fragment exterior to viral membrane, a
PT stabilising peptide, and, optionally, viral cell surface receptor or its
PT fragment.

XX Example 12; Page 65; 84pp; English.

CC The invention relates to methods of generating immunogens that elicit
CC neutralising antibodies which target regions of viral envelope proteins
CC such as the gp120/gp41 glycoprotein 120(glycoprotein 41) complex of HIV-
CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and
CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-
CC helical regions of the ectodomain of the HIV-1 transmembrane protein to
CC stabilise fusion-active intermediate structures, which can be used as
CC vaccine immunogens. Immunogenic compositions comprise a viral envelope
CC protein or its fragment exterior to the viral membrane, a stabilising
CC peptide to disrupt formation of structural intermediates necessary for
CC viral fusion and entry, and optionally, a viral cell surface receptor or
CC its fragment. The stabilising peptide is capable of associating with the
CC envelope protein or its fragment to form a stabilised, fusion active
CC structure. Antibody binding assays are used to determine the ability of
CC immunogen vaccines to generate an immune response to various forms of
CC envelope. Virus neutralisation assays can be used to characterise the
CC antibody response raised against HIV-1 gp41 domains. The sequences and
CC methods are useful for inhibiting HIV infection, for inducing an immune
CC response in an animal and for raising antibodies

XX Sequence 7 AA;

Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 29
AAG63975
ID AAG63975 standard; peptide; 7 AA.
XX AAG63975;
XX 11-SEP-2003 (revised)
DT 13-NOV-2001 (first entry)
XX Amino acid sequence of a HIV-1 gp41 derived peptide.
DE Nonstructural gene; NS gene; influenza A virus; NS1 gene; vaccine;
KW viral infection; influenza infection; HIV-1 infection; gp41.
XX Human immunodeficiency virus 1.
XX WO200164860-A2.
XX 07-SEP-2001.
XX 02-MAR-2001; 2001WO-EP002392.
XX 02-MAR-2000; 2000EP-00104338.
XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX Ferko B, Egorov A, Voglauer R;
XX WPI; 2001-514840/56.
XX Recombinant NS gene of an influenza A virus comprising a functional RNA
PT binding domain and a gene sequence modification after nucleotide position
PT 400 of the NS1 gene segment, useful for producing a live attenuated
PT influenza virus vaccine.
XX Claim 3; Page 25; 40pp; English.
XX The specification describes a recombinant nonstructural (NS) gene of an
CC influenza A virus. The gene comprises a functional RNA binding domain and
CC a gene sequence modification after nucleotide position 400 of the NS1
CC gene segment counted on the basis of influenza A/PR/8/34 virus, where
CC the modification bars transcription of the remaining portion of the NS1

CC gene segment. The recombinant NS gene is used to produce a vaccine, which
 CC is useful for prophylactic or therapeutic application against a viral
 CC infection, preferably against influenza or HIV-1 infection. Influenza
 CC virus transfectants that contain the modified NS gene may have an
 CC interferon (IFN) inducing phenotype, but may or may not be sensitive
 CC towards to IFN. The present sequence represents a gp11 epitope, and was
 CC used to modify the NS genes of the invention. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 CC
 XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 30
 AAU80301
 ID AAU80301 standard; peptide; 7 AA.

XX AC AAU80301;

XX DT 29-AUG-2003 (revised)
 XX DT 15-JUL-2002 (first entry)

XX DE HIV-1 canonical epitope peptide sequence.

XX KW Canonical epitope; fusion protein; antigenic determinant; vaccine;
 KW capsid protein of potato virus X; PVX; CPV; viral hepatitis;
 KW human immunodeficiency virus; HIV; hepatitis C virus; HCV;
 KW Epstein-Barr virus; EBV; influenza virus; antibacterial; anti-HIV;
 KW acquired immunodeficiency syndrome; AIDS; virucide; hepatotropic.

XX OS Human immunodeficiency virus 1.

XX PN EPI167530-A2.

XX PD 02-JAN-2002.

XX PF 11-JUN-2001; 2001EP-00202225.

XX PR 16-JUN-2000; 2000IT-RM000327.

XX PA (CNEH) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
 XX PA (SUPR-) INST SUPERIORE DI SANITA.

XX PI Benvenuto E, Marusic C, Belardelli F, Rizza P, Capone I;

XX DR WPI; 2002-180948/24.

XX DR N-PSDB; ABKS0054.

XX PT Novel fusion protein, useful for treating e.g., HIV-1 and influenza
 XX PT virus, comprises an amino terminal antigenic determinant portion of e.g.,
 XX PT influenza virus, fused to carboxy terminal portion comprising capsid
 XX PT protein of potato virus X.

XX PS Claim 4; SEQ ID NO 1; 22pp; English.

XX CC The present invention relates to a new fusion protein with an amino
 CC terminal portion comprising an antigenic determinant and a carboxy
 CC terminal portion comprising the capsid protein of potato virus X (PVX)
 CC (CPV) or its variant. The amino terminal portion is fused to the carboxy
 CC terminal portion in such a way that the antigenic determinant is in frame
 CC with CPV or its variant. The molecules of the invention are useful for
 CC preparing a pharmaceutical composition for treating a pathology
 CC associated with bacterial or viral pathogenic agent such as human
 CC immunodeficiency virus (HIV), hepatitis C virus (HCV), Epstein-Barr virus
 CC (EBV) or influenza virus. The medicaments prepared using the molecules of
 CC the invention are useful for treating infectious diseases, preferably

CC acquired immunodeficiency syndrome (AIDS), viral hepatitis, influenza and
 CC other pathology associated with EBV virus. The present amino acid
 CC sequence represents the HIV canonical epitope that was used in the
 CC methods of the invention as a fusion protein, as described above. Note:
 CC The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office. (Updated on 29-AUG-2003 to standardise OS field)
 CC
 XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 1 ELDKWA 6

RESULT 31
 AAU99586
 ID AAU99586 standard; peptide; 7 AA.

XX AC AAU99586;

XX DT 21-OCT-2002 (first entry)

XX DE Epitope of neutralising antibody 2F5.

XX KW Stable immunogenic proteoliposome; ellipsoid shape; spherical shape;
 KW transmembrane protein; lipid membrane; viral envelope glycoprotein;
 KW immune reaction; human immunodeficiency virus infection; HIV; 2F5;
 KW antibody library; immunostimulant; virucide; neutralising antibody.

XX OS Unidentified.

XX PN WO200256831-A2.

XX PD 25-JUL-2002.

XX PF 27-DEC-2001; 2001WO-US050820.

XX PR 27-DEC-2000; 2000US-0258438P.

XX PA (DAND) DANA FARBER CANCER INST INC.

XX PI Wyatt RT, Sodroski JG, Mirzabekov T, Grunder C;

XX DR WPI; 2002-583669/62.

XX PT New stable immunogenic proteoliposome containing a transmembrane protein,
 XX PT useful as an immunogen for eliciting immune reaction (e.g. against an HIV
 XX PT infection), in drug screening assays or for identifying ligands.

XX PS Example 1; Page 49; 92pp; English.

XX CC The present invention relates to stable immunogenic proteoliposomes,
 CC comprising a spherical or ellipsoid shape, having a ligand to an
 CC immunogenic transmembrane protein anchored to the shape, and an isolated
 CC integral membrane protein bound to the ligand. The shape's surface is
 CC surrounded by a lipid membrane. The integral membrane protein's
 CC transmembrane domains are in the lipid membrane. The immunogenic
 CC transmembrane protein is a multimer and has a wild type conformation. The
 CC proteoliposome preferably contains a transmembrane protein such as a
 CC viral envelope glycoprotein. The shape preferably contains an attractant
 CC such as streptavidin or avidin and the lipid membrane contains a moiety
 CC that binds to the attractant such as biotin. The proteoliposomes are
 CC useful as immunogens for eliciting an immune reaction, e.g. against human
 CC immunodeficiency virus (HIV) infection. They are also useful in screening
 CC assays (e.g. as antigens for screening antibody libraries), drug
 CC screening, and for identifying ligands. The present sequence for an
 CC epitope of the neutralising antibody 2F5 is used in the examples of the
 CC present invention

```
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 35; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 32
AAU97480
ID AAU97480 standard; peptide; 7 AA.
XX AC AAU97480;
XX DT 29-AUG-2003 (revised)
XX DT 13-AUG-2002 (first entry)
XX DE HIV-1 infection inhibitory activity associated peptide #3.
XX KW Human immunodeficiency virus; HIV; antisense peptide; gp41; T20;
XX KW infection inhibitory activity; envelope glycoprotein; gp160;
XX KW infection inhibition; HIV-1_1_1B; infection mechanism; virucide;
XX KW anti-HIV; HIV-antagonist.
XX OS Human immunodeficiency virus 1.
XX PN JP200208099-A.
XX PD 27-MAR-2002.
XX PF 13-SEP-2000; 2000JP-00277747.
XX PR 13-SEP-2000; 2000JP-00277747.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2002-430873/46.
XX PT Antisense peptides with HIV-1 infection inhibitory activity having gp41
XX PT amino acid sequence in T20 of HIV-1 envelope glycoprotein gp160 molecules
XX PT useful for investigation of infection mechanism of HIV-1.
XX PS Example B; Page 9; 16pp; Japanese.
XX CC The present invention relates to new antisense peptides with HIV-1
XX CC infection inhibitory activity having gp41 amino acid sequence in T20 of
XX CC HIV-1 envelope glycoprotein gp160 molecules. The peptides of the
XX CC invention are useful for infection inhibition of HIV-1_1_1B. The
XX CC invention is advantageous as it can be used for treatment of HIV-1 and
XX CC investigation of its infection mechanism. The present amino acid sequence
XX CC represents one of a collection (AAU97478-AAU97487) of human
XX CC immunodeficiency virus (HIV-1) infection inhibitory activity associated
XX CC peptides. (Updated on 29-AUG-2003 to standardise OS field)
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 35; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 33
ABR39671
ID ABR39671 standard; peptide; 7 AA.
XX
```

```
AC ABR39671;
XX DT 23-OCT-2003 (revised)
XX DT 23-JUN-2003 (first entry)
XX DE HIV-1 gp41 peptide fragment.
XX KW HIV-1; immune response; gp41; anti-HIV; vaccine; mAb 4E10-IgG1;
XX KW anti-idiopathic antibody.
XX OS Human immunodeficiency virus 1.
XX PN WO2003022879-A2.
XX PD 20-MAR-2003.
XX PF 09-SEP-2002; 2002WO-EP010070.
XX PR 07-SEP-2001; 2001US-0318091P.
XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX PI Stiegler G, Kunert R, Katinger H;
XX DR WPI; 2003-354526/33.
XX CC New peptide that interferes with HIV-1 entry into target cells and
XX CC preferably induces an HIV-1 neutralizing immune response, where the
XX CC peptide is a fragment of gp41 of HIV-1, useful for inhibiting or
XX CC preventing HIV-1 infection.
XX PS Example 7; Page 20; 33pp; English.
XX CC The invention relates to a peptide that interferes with HIV-1 entry into
XX CC target cells and preferably induces an HIV-1 neutralizing immune
XX CC response, where the peptide is a fragment of gp41 of HIV-1. The peptide,
XX CC antibody, composition and vaccine are useful for inhibiting or preventing
XX CC HIV-1 infection. The mAb 4E10-IgG1 is useful for eliciting or screening
XX CC for an anti-idiopathic antibody that is reactive with the 4E10 binding
XX CC paratope of mAb 4E10-IgG1, and that preferably mimics a fragment of gp41
XX CC of HIV. Sequences ABR39667-675 represent HIV-1 gp41 peptide fragments.
XX CC (Updated on 23-OCT-2003 to standardise OS field)
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 35; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 34
ABR62950
ID ABR62950 standard; peptide; 7 AA.
XX AC ABR62950;
XX DT 04-DEC-2003 (first entry)
XX DE HIV-1 virus envelope ectodomain gp41 core epitope variant.
XX KW HIV-1; anti-idiotype; antibody; anti-HIV; virucide; vaccine.
XX OS Synthetic.
XX PN WO2003059953-A2.
XX PD 24-JUL-2003.
XX PR 17-JAN-2003; 2003WO-EP000455.
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XX PR 17-JAN-2002; 2002EP-00001250.
XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX PI Kunert R, Weik R, Stiegler G, Katinger H;
XX DR WPI; 2003-598509/56.
XX
XX PT New anti-idiotypic antibody inducing HIV-1 neutralizing antibodies,
XX PT useful as a screening tool or diagnostic agent, and for the manufacture
XX PT of a vaccine, for prophylactic or therapeutic application against HIV-1
XX PT infection.
XX
XX FS Claim 2; Page 15; 32pp; English.
XX
XX CC The present sequence is that of a variant of a highly conserved epitope
XX CC sequence (see ABR62944) on the HIV-1 envelope ectodomain gp41. The
XX CC invention provides an antibody, or its fragment, which is reactive with
XX CC HIV-1 neutralising antibody 2F5 (ECACC 90091704) and which inhibits or
XX CC prevents the HIV-1 neutralisation activity of 2F5 and/or the binding of
XX CC 2F5 to HIV-1 gp41. The antibody preferably inhibits or prevents the
XX CC binding of 2F5 to proteins or peptides that comprise the HIV-1 gp41
XX CC conserved epitope or its variants (see ABR62945-55). Upon administration
XX CC to a mammal, the antibody elicits Ab3-type antibodies that have HIV-1
XX CC neutralising activity and/or that compete with 2F5 for binding to
XX CC proteins comprising the conserved epitope or its variants. The antibody
XX CC is preferably an Ab2-type antibody which is anti-idiotypic to 2F5, is
XX CC monoclonal and is produced by hybridoma cell line 3G6 (ECACC 01100279),
XX CC or is a chimeric or humanized antibody. The antibody or its fragment may
XX CC be coupled, linked or fused to an immunoreactive molecule, such as
XX CC interleukin-4 or interleukin-15, that increases or intensifies a B cell
XX CC response. It can be used as a screening tool, diagnostic or therapeutic
XX CC agent, or as a vaccine against HIV-1 infection.
XX
XX SQ Sequence 7 AA;
XX
XX Query Match 100.0%; Score 35; DB 7; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ELDKWA 6
XX Db 1 ELDKWA 6
XX
XX RESULT 35
XX ABR62947
XX ID ABR62947 standard; peptide; 7 AA.
XX AC ABR62947;
XX AS
XX DT 04-DEC-2003 (first entry)
XX DE HIV-1 virus envelope ectodomain gp41 core epitope variant.
XX KW HIV-1; anti-idiotypic; antibody; anti-HIV; virucide; vaccine.
XX OS Synthetic.
XX
XX WO2003059953-A2.
XX PN
XX PD 24-JUL-2003.
XX
XX PF 17-JAN-2003; 2003WO-EP000455.
XX PT
XX PR 17-JAN-2002; 2002EP-00001250.
XX
XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX PI Kunert R, Weik R, Stiegler G, Katinger H;
XX DR WPI; 2003-598509/56.
XX
XX Query Match 100.0%; Score 35; DB 7; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 ELDKWA 6
XX Db 1 ELDKWA 6
XX
XX RESULT 36
XX AAR71632
XX ID AAR71632 standard; peptide; 8 AA.
XX AC AAR71632;
XX AS
XX DT 25-MAR-2003 (revised)
XX DT 20-SEP-1995 (first entry)
XX DE HIV-1 gp41 peptide.
XX KW HIV-1; gp41; gp160; 2F5 epitope; antibody; cell fusion; AIDS; vaccine;
XX KW immunogen; therapy; human immunodeficiency virus type 1;
XX KW monoclonal antibody; Mab.
XX OS Synthetic.
XX
XX WO9507354-A1.
XX PN
XX PD 16-MAR-1995.
XX
XX PF 12-SEP-1994; 94WO-EP003039.
XX PR 11-SEP-1993; 93EP-00114631.
XX
XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
XX PI Katinger H, Muster T;
XX DR WPI; 1995-123428/16.
XX
XX PT New peptide(s) corresponding to a HIV-1 gp 160 epitope - used to elicit
XX PT antibodies which neutralise different HIV-1 strains and inhibit cell
XX PT fusion caused by HIV-1.
XX

```

PS Claim 1; Page 17; 28pp; English.

XX The peptides given in AAR71631-36 are based on amino acids 661-668 of HIV

CC -1 isolate BH10 gp41, the epitope of human Mab 2F5. The peptides may be

CC inserted into antigenic sites of a viral protein, e.g. influenza virus

CC hemagglutinin, by gene fusion, for HIV-1 vaccine development. (Updated on

CC 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA;

SQ

Query Match 100.0%; Score 35; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

QY 1 ELDKWA 6

DB 2 ELDKWA 7

RESULT 37

AAV05254

ID AAY05254 standard; peptide; 8 AA.

XX AC AAY05254;

DT 17-OCT-2003 (revised)

DT 21-JUN-1999 (first entry)

DE MN-HIV gp41 fragment.

XX HIV; gp41; viral load reduction; viral titre reduction; HIV infection;

KW immunogenic carrier; vaccine; therapy.

XX Human immunodeficiency virus 1.

OS WO9917789-A1.

XX 15-APR-1999.

XX 06-OCT-1998; 98WO-US020966.

XX 07-OCT-1997; 97US-00946525.

XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.

PA Rubinstein A, Bloom BR, Devash Y, Cryz SJ;

PI WPI; 1999-263900/22.

DR Reducing load of human immune deficiency virus.

FT

XX Claim 3; Page 11; 144pp; English.

XX This sequence represents a fragment from the gp41 protein of the MN

CC strain of HIV. The invention relates to a method for reducing the level

CC of HIV (human immune deficiency virus) titre in a mammal, by

CC administering a composition (A) containing at least one peptide (such as

CC this sequence) coupled to an immunogenic carrier. (A) are used to treat

CC or prevent HIV infections, including prevention of maternal-fetal

CC transfer. (A) induces a long-term neutralising antibody response in the

CC serum; high levels of mucosal antibodies and cytotoxic T cells, and thus

CC reduces viral load and prevents or inhibits progression of disease.

CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 8 AA;

SQ

Query Match 100.0%; Score 35; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6

DB 3 ELDKWA 8

RESULT 38

ABP12065

ID ABP12065 standard; peptide; 8 AA.

XX AC ABP12065;

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX HIV A02 super motif env peptide #122.

DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

OS WO200124810-A1.

XX 12-APR-2001.

PD 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

XX (EPIM-) EPIMUNE INC.

PA Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cellis E, Kubo RT, Grey HW;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX Claim 32; Page 116; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC in whole antigens can be avoided with the use of group-based vaccines. An

CC additional advantage of an group-based vaccine approach is the ability to

CC combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP1501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 8 AA;

SQ

Query Match 100.0%; Score 35; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. NO. 1.4e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0;

QY 1 ELDKWA 6

DB 1 ELDKWA 6

```

RESULT 39
ID ABP12063
AC ABP12063 standard; peptide; 8 AA.
XX
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif env peptide #120.
XX
XX HIV, HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
XX vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US027766.
XX
XX 05-OCT-1999; 99US-00412863.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32; Page 116; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
XX be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines. An
XX additional advantage of an group-based vaccine approach is the ability to
XX combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 35; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 3 ELDKWA 8

RESULT 40
ID ABP15180
AC ABP15180 standard; peptide; 8 AA.
XX
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #60.
XX
XX HIV, HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
XX vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US027766.
XX
XX 05-OCT-1999; 99US-00412863.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32; Page 180; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
XX be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines. An
XX additional advantage of an group-based vaccine approach is the ability to
XX combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 35; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 41
ID ABP20177
AC ABP20177 standard; peptide; 8 AA.
XX
XX

```

AC ABP20177;
XX 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
XX HIV A03 motif env peptide #381.
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200124810-A1.
XX
XX 12-APR-2001.
PD
XX 05-OCT-2000; 2000WO-US027766.
PF
XX 05-OCT-1999; 99US-00412863.
XX
XX (EPTM-) EPIMMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32; Page 283; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 35; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 3 ELDKWA 8
RESULT 42
AAU97481
ID AAU97481 standard; peptide; 8 AA.
XX
XX AAU97481;
AC
XX

DT 29-AUG-2003 (revised)
DT 13-AUG-2002 (first entry)
XX
XX HIV-1 infection inhibitory activity associated peptide #4.
XX
XX Human immunodeficiency virus; HIV; antisense peptide; gp41; T20;
KW infection inhibitory activity; envelope glycoprotein; gp160;
KW infection inhibitor; HIV-1_1_1B; infection mechanism; virucide;
KW anti-HIV; HIV-antagonist.
XX
XX Human immunodeficiency virus 1.
OS
XX JP2002088099-A.
XX
XX 27-MAR-2002.
PD
XX 13-SEP-2000; 2000JP-00277747.
PF
XX 13-SEP-2000; 2000JP-00277747.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA
XX WPI; 2002-430873/46.
XX
XX Antisense peptides with HIV-1 infection inhibitory activity having gp41
PT amino acid sequence in T20 of HIV-1 envelope glycoprotein gp160 molecules
PT useful for investigation of infection mechanism of HIV-1.
XX
XX Example B; Page 9; 16pp; Japanese.
PS
XX The present invention relates to new antisense peptides with HIV-1
CC infection inhibitory activity having gp41 amino acid sequence in T20 of
CC HIV-1 envelope glycoprotein gp160 molecules. The peptides of the
CC invention are useful for infection inhibition of HIV-1_1_1B. The
CC invention is advantageous as it can be used for treatment of HIV-1 and
CC investigation of its infection mechanism. The present amino acid sequence
CC represents one of a collection (AAU97478-AAU97487) of human
CC immunodeficiency virus (HIV-1) infection inhibitory activity associated
CC peptides. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 35; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 2 ELDKWA 7
RESULT 43
ABR62953
ID ABR62953 standard; peptide; 8 AA.
XX
XX ABR62953;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX HIV-1 virus envelope ectodomain gp41 core epitope variant.
DE
XX HIV-1; anti-idiotypic; antibody; anti-HIV; virucide; vaccine.
KW
XX Synthetic.
OS
XX WO2003059953-A2.
XX
XX 24-JUL-2003.
PD
XX 17-JAN-2003; 2003WO-EP000455.
XX
XX 17-JAN-2002; 2002EP-00001250.
XX

PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
 XX
 PI Kunert R, Weik R, Stiegler G, Katinger H;
 XX
 DR WPI; 2003-598509/56.
 XX
 XX New anti-idiotypic antibody inducing HIV-1 neutralizing antibodies,
 PT useful as a screening tool or diagnostic agent, and for the manufacture
 PT of a vaccine, for prophylactic or therapeutic application against HIV-1
 PT infection.
 XX
 XX Claim 2; Page 15; 32pp; English.
 XX
 CC The present sequence is that of a variant of a highly conserved epitope
 CC sequence (see ABR62944) on the HIV-1 envelope ectodomain gp41. The
 CC invention provides an antibody, or its fragment, which is reactive with
 CC HIV-1 neutralising antibody 2F5 (ECACC 90091704) and which inhibits or
 CC prevents the HIV-1 neutralisation activity of 2F5 and/or the binding of
 CC 2F5 to HIV-1 gp41. The antibody preferably inhibits or prevents the
 CC binding of 2F5 to proteins or peptides that comprise the HIV-1 gp41
 CC conserved epitope or its variants (see ABR62945-55). Upon administration
 CC to a mammal, the antibody elicits Ab3-type antibodies that have HIV-1
 CC neutralising activity and/or that compete with 2F5 for binding to
 CC proteins comprising the conserved epitope or its variants. The antibody
 CC is preferably an Ab2-type antibody which is anti-idiotypic to 2F5, is
 CC monoclonal and is produced by hybridoma cell line 3G6 (ECACC 01100279),
 CC or is a chimeric or humanized antibody. The antibody or its fragment may
 CC be coupled, linked or fused to an immunoreactive molecule, such as
 CC interleukin-4 or interleukin-15, that increases or intensifies a B cell
 CC response. It can be used as a screening tool, diagnostic or therapeutic
 CC agent, or as a vaccine against HIV-1 infection
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 100.0%; Score 35; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 Db |||||
 2 ELDKWA 7
 RESULT 44
 AAR71637
 ID AAR71637 standard; peptide; 9 AA.
 XX
 AC AAR71637;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 XX Immunization control peptide.
 DE
 XX HIV-1; gp41; gp160; 2F5 epitope; antibody; cell fusion; AIDS; vaccine;
 KW immunogen; therapy; human immunodeficiency virus type 1;
 KW monoclonal antibody; Mab; hemagglutinin; baculovirus; Sf9;
 KW Spodoptera frugiperda.
 XX
 OS Synthetic.
 OS WO9507354-A1.
 XX
 XX 16-MAR-1995.
 XX
 PF 12-SEP-1994; 94WO-EP0030339.
 XX
 PR 11-SEP-1993; 93EP-00114631.
 XX
 XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
 XX
 PI Katinger H, Muetter T;
 XX
 DR WPI; 1995-123428/16.
 XX
 PT New peptide(s) corresponding to a HIV-1 gp 160 epitope - used to elicit
 PT antibodies which neutralise different HIV-1 strains and inhibit cell
 PT fusion caused by HIV-1.
 XX
 XX Example 5; Page 15; 28pp; English.
 PS
 XX Chimeric hemagglutinins carrying extended human MAb 2F5 epitopes
 CC (AAR71631-36) were expressed by recombinant baculovirus in Sf9 cells. The
 CC antibody response of mice immunized by these Sf9 cells was tested using
 CC the peptide given in AAR71637 as a control. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 35; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 Db |||||
 4 ELDKWA 9
 RESULT 45
 AAW99914
 ID AAW99914 standard; peptide; 9 AA.
 XX
 AC AAW99914;
 XX
 DT 05-MAY-1999 (first entry)
 DT
 XX HIV-1 vaccine synthetic peptide #3.
 DE
 XX HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
 KW gag protein; B-cell epitope; gp41 protein; chimeric; infection.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.
 XX
 XX US5876731-A.
 FN
 XX 02-MAR-1999.
 PD
 XX 05-JUN-1995; 95US-00462507.
 PF
 XX 09-JUN-1993; 93US-00073378.
 PR
 XX 09-JUN-1994; 94US-00257528.
 PR
 XX (CONN-) CONNAUGHT LAB LTD.
 PA
 XX Chong P, Klein MH, Sia CDY;
 PI
 XX WPI; 1999-189590/16.
 DR
 XX Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
 PT epitope linked to gp41 B-cell epitope.
 PT
 XX Claim 7; Col 72; 41pp; English.
 XX
 FS
 XX The present invention describes a synthetic peptide comprising an amino
 CC acid sequence containing a T-cell epitope of an HIV gag protein linked at
 CC its C terminus to an amino acid sequence containing a B-cell epitope of
 CC an HIV gp41 protein and containing the amino acid sequence: xLKDWX2;
 CC where X1 = E, A, G or Q, and X2 = A or T, or an amino acid sequence
 CC capable of eliciting an HIV-specific antiserum and recognizing the
 CC sequence xLKDWX2. The synthetic peptide is useful in vaccines against
 CC HIV infection and in diagnostic applications. AAW98892 to AAW98906, and
 CC AAW98899 to AAW99989 represent synthetic peptides from the present
 CC invention
 XX
 XX Sequence 9 AA;
 SQ

Thu Mar 18 10:20:33 2004

Query Match 100.0%; Score 35; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
DB 4 ELDKWA 9

RESULT 46
ABP20096
ID ABP20096 standard; peptide; 9 AA.
XX
AC ABP20096;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif env peptide #300.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HW;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 281; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 9 AA;
Query Match 100.0%; Score 35; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
DB 4 ELDKWA 9

RESULT 47
ABP15290
ID ABP15290 standard; peptide; 9 AA.
XX
AC ABP15290;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #170.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HW;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 182; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 9 AA;
Query Match 100.0%; Score 35; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  ELDKWA 6
Db      1  ELDKWA 6

RESULT 48
ABP12211
ID  ABP12211 standard; peptide; 9 AA.
XX
AC  ABP12211;
XX
DT  11-SEP-2003 (revised)
DT  15-JUL-2002 (first entry)
XX
DE  HIV A02 super motif env peptide #268.
XX
KW  HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW  vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW  vaccine; HIV infection; immunisation; virucide.
XX
OS  Human immunodeficiency virus 1.
XX
PN  WO200124810-A1.
XX
PD  12-APR-2001.
XX
PF  05-OCT-2000; 2000WO-US027766.
XX
PR  05-OCT-1999; 99US-00412863.
XX
PA  (EPIM-) EPIMMUNE INC.
XX
PI  Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI  Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR  WPI; 2001-354887/37.
XX
PT  Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT  peptide groups, useful for vaccinating against HIV-1.
XX
PS  Claim 32; Page 119; 448pp; English.
XX
CC  The present invention describes a composition (I) comprising a prepared
CC  human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC  sequence selected from 51 defined amino acid sequences (ABL25347 to
CC  ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC  be used for immunising subjects against HIV-1 infections. The use of
CC  group-based vaccines has several advantages over traditional vaccines,
CC  particularly when compared to the use of whole antigens in vaccine
CC  compositions. There is evidence that the immune response to whole
CC  antigens is directed largely toward variable regions of the antigen,
CC  allowing for immune escape due to mutations. The groups for inclusion in
CC  an group-based vaccine may be selected from conserved regions of viral or
CC  tumour-associated antigens, which therefore reduces the likelihood of
CC  escape mutants. Furthermore, immunosuppressive groups that may be present
CC  in whole antigens can be avoided with the use of group-based vaccines. An
CC  additional advantage of an group-based vaccine approach is the ability to
CC  combine selected groups (CTL and HTL), and further, to modify the
CC  composition of the groups, achieving, for example, enhanced
CC  immunogenicity. Accordingly, the immune response can be modulated, as
CC  appropriate, for the target disease. Similar engineering of the response
CC  is not possible with traditional approaches. ABP11501 to ABP25412
CC  represent peptide sequences used in the exemplification of the present
CC  invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ  Sequence 9 AA;

Query Match      100.0%; Score 35; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELDKWA 6
Db      1  ELDKWA 6

RESULT 49
ABP18573
ID  ABP18573 standard; peptide; 9 AA.
XX
AC  ABP18573;
XX
DT  11-SEP-2003 (revised)
DT  15-JUL-2002 (first entry)
XX
DE  HIV BG2 super motif env peptide #148.
XX
KW  HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW  vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW  vaccine; HIV infection; immunisation; virucide.
XX
OS  Human immunodeficiency virus 1.
XX
PN  WO200124810-A1.
XX
PD  12-APR-2001.
XX
PF  05-OCT-2000; 2000WO-US027766.
XX
PR  05-OCT-1999; 99US-00412863.
XX
PA  (EPIM-) EPIMMUNE INC.
XX
PI  Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI  Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR  WPI; 2001-354887/37.
XX
PT  Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT  peptide groups, useful for vaccinating against HIV-1.
XX
PS  Claim 32; Page 249; 448pp; English.
XX
CC  The present invention describes a composition (I) comprising a prepared
CC  human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC  sequence selected from 51 defined amino acid sequences (ABL25347 to
CC  ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC  be used for immunising subjects against HIV-1 infections. The use of
CC  group-based vaccines has several advantages over traditional vaccines,
CC  particularly when compared to the use of whole antigens in vaccine
CC  compositions. There is evidence that the immune response to whole
CC  antigens is directed largely toward variable regions of the antigen,
CC  allowing for immune escape due to mutations. The groups for inclusion in
CC  an group-based vaccine may be selected from conserved regions of viral or
CC  tumour-associated antigens, which therefore reduces the likelihood of
CC  escape mutants. Furthermore, immunosuppressive groups that may be present
CC  in whole antigens can be avoided with the use of group-based vaccines. An
CC  additional advantage of an group-based vaccine approach is the ability to
CC  combine selected groups (CTL and HTL), and further, to modify the
CC  composition of the groups, achieving, for example, enhanced
CC  immunogenicity. Accordingly, the immune response can be modulated, as
CC  appropriate, for the target disease. Similar engineering of the response
CC  is not possible with traditional approaches. ABP11501 to ABP25412
CC  represent peptide sequences used in the exemplification of the present
CC  invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ  Sequence 9 AA;

Query Match      100.0%; Score 35; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELDKWA 6
Db      1  ELDKWA 6

```


RESULT 50
AAB38721
ID AAB38721 standard; peptide; 10 AA.
XX
AC AAB38721;
XX
DT 02-FEB-2001 (first entry)
XX
DE HIV-1 peptide epitope #74.
XX
KW Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX
OS Human immunodeficiency virus.
XX
PW WO200058438-A2.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-US008232.
XX
PR 29-MAR-1999; 99US-0126938P.
XX
PA (BERN/) BERNSTEIN D.
PA (CHOW/) CHOWDHURY A.
PA (KOZH/) KOZHICH A.
PA (MOTS/) MOTSENBOCKER M.
XX
PI Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
XX
DR WPI; 2000-656164/63.
XX
PT Synthetic peptides useful for preventing and treating HIV infection in
PT mammals, comprising a conformationally constrained portion and a portion
PT with continuous stretch of amino acids of predicted secondary structure.
XX
PS Disclosure; Page 11; 69pp; English.
XX
CC The present invention relates to peptides (AAB38648-B38970) comprising a
CC first conformationally constrained portion with a cross-linked group of a
CC HIV envelope protein that induces neutralising antibodies, and a second
CC portion comprising a continuous stretch of at least 5 amino acids having
CC a predicted secondary structure. The present sequence is one such
CC peptide. The peptides of the present invention are useful as a vaccine
CC for prophylactic or therapeutic treatment of a mammal for HIV infection
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 35; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.6; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 ELDKWA 6
Db 3 ELDKWA 8
|||||
Search completed: March 16, 2004, 09:16:28
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2004, 09:12:35 ; Search time 21 Seconds
(without alignments)
27.483 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR 78:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	357	2 S21994	envelope protein g
2	35	100.0	357	2 S21996	envelope protein g
3	35	100.0	357	2 S21992	envelope protein g
4	35	100.0	358	2 S21998	envelope protein g
5	35	100.0	443	2 C41621	envelope protein p
6	35	100.0	445	2 A41621	env polypeptide M
7	35	100.0	464	2 S59898	kynureninase (EC 3
8	35	100.0	464	2 T48675	kynureninase (EC 3
9	35	100.0	465	2 G02652	kynureninase (EC 3
10	35	100.0	817	2 T16409	hypothetical prote
11	35	100.0	846	1 VCLJND	env polypeptide pr
12	35	100.0	847	2 T09448	envelope glycoprot
13	35	100.0	847	2 S13289	env protein - huma
14	35	100.0	851	2 S33985	env polypeptide -
15	35	100.0	852	1 VCLJBR	env polypeptide -
16	35	100.0	852	2 T12016	envelope glycoprot
17	35	100.0	853	2 S54384	envelope polypept
18	35	100.0	854	2 S13288	env protein - huma
19	35	100.0	855	1 VCLJAJ	env polypeptide pr
20	35	100.0	855	1 VCLJZR	env polypeptide pr
21	35	100.0	856	1 VCLJH3	env polypeptide pr
22	35	100.0	856	1 VCLJVL	env polypeptide pr
23	35	100.0	856	1 VCLJ3W	env polypeptide pr
24	35	100.0	859	1 VCLJWN	env polypeptide pr
25	35	100.0	859	2 T01672	envelope polypept
26	35	100.0	861	1 VCLJIV	env polypeptide pr
27	35	100.0	861	1 VCLJSC	env polypeptide pr
28	35	100.0	926	1 RDSFNH	nitrate reductase
29	32	91.4	268	2 T02448	hypothetical prote

30	32	91.4	326	2 E71561	probable solute pr
31	32	91.4	332	2 D71274	probable prolipop
32	32	91.4	448	2 C83347	probable dipeptida
33	32	91.4	501	2 S51160	nitrate reductase
34	32	91.4	617	2 S19254	nitrate reductase
35	32	91.4	868	1 VCLJH4	env polypeptide -
36	32	91.4	889	2 T02240	nitrate reductase
37	32	91.4	912	1 RDBHNS	nitrate reductase
38	32	91.4	915	1 RDBHNS	nitrate reductase
39	32	91.4	916	2 S07554	nitrate reductase
40	32	91.4	1707	2 S77910	hypothetical prote
41	32	88.6	78	2 E82798	hypothetical prote
42	31	88.6	112	2 C64746	yafu protein - Esc
43	31	88.6	126	2 H70387	hypothetical prote
44	31	88.6	151	2 AB0550	conserved hypotet
45	31	88.6	152	2 AH0368	conserved hypotet
46	31	88.6	201	2 A45332	zipper protein - c
47	31	88.6	229	2 AF1167	ABC transporter, A
48	31	88.6	248	2 B83030	probable rRNA meth
49	31	88.6	338	2 T33683	hypothetical prote
50	31	88.6	343	2 T20280	hypothetical prote
51	31	88.6	358	2 S22002	envelope protein g
52	31	88.6	358	2 S22000	envelope protein g
53	31	88.6	358	2 S70417	envelope protein g
54	31	88.6	392	2 B98080	galactokinase (EC
55	31	88.6	392	2 D95216	galactokinase (imp
56	31	88.6	418	2 JC7872	stearyl-CoA 9-des
57	31	88.6	483	2 A11908	hypothetical prote
58	31	88.6	500	1 A44001	gag polypeptide -
59	31	88.6	502	1 F0VWA2	gag polypeptide -
60	31	88.6	564	2 F59092	hypothetical prote
61	31	88.6	573	2 T05328	hypothetical prote
62	31	88.6	706	2 AD0173	conserved hypotet
63	31	88.6	719	2 T52510	hypothetical prote
64	31	88.6	733	2 S76856	hypothetical prote
65	31	88.6	745	2 B84673	hypothetical prote
66	31	88.6	752	2 F81203	maltoase phosphory
67	31	88.6	752	2 C81781	probable maltose p
68	31	88.6	785	2 S73098	aminopeptidase (EC
69	31	88.6	826	2 E90289	malate synthase, p
70	31	88.6	854	1 VCLJSI	env polypeptide pr
71	31	88.6	863	2 A53034	gag polypeptide -
72	31	88.6	877	2 S45197	envelope protein p
73	31	88.6	880	1 SYBSVS	valine-tRNA ligase
74	31	88.6	881	2 S25445	nitrate reductase
75	31	88.6	884	2 S66308	nitrate reductase
76	31	88.6	886	2 A59223	nitrate reductase
77	31	88.6	1022	2 I53078	homeotic gene regu
78	31	88.6	1055	1 A37205	leukotoxin A - Act
79	31	88.6	1235	1 VGIHMJ	E2 glycoprotein pr
80	31	88.6	1257	2 T28937	hypothetical prote
81	31	88.6	1324	1 VGIHS9	E2 glycoprotein pr
82	31	88.6	1376	1 VGIHJ2	E2 glycoprotein pr
83	31	88.6	1376	1 JQ1534	E2 glycoprotein pr
84	31	88.6	1572	2 S45251	SNFalpha protein
85	31	88.6	1586	2 S39580	HBRM protein - hum
86	31	88.6	1613	2 S39059	protein BRG1 - hum
87	31	88.6	1647	2 S45252	SNF2beta protein -
88	30	85.7	120	2 F96658	hypothetical prote
89	30	85.7	166	2 T50531	hypothetical prote
90	30	85.7	167	2 S76890	hypothetical prote
91	30	85.7	314	2 T42604	probable uracil-DN
92	30	85.7	325	2 T03010	probable replicati
93	30	85.7	327	2 AF0618	conserved hypotet
94	30	85.7	336	2 PC1139	hypothetical prote
95	30	85.7	339	2 AC2153	hypothetical prote
96	30	85.7	357	2 S22006	envelope protein g
97	30	85.7	357	2 S22004	envelope protein g
98	30	85.7	430	2 S75701	hypothetical prote
99	30	85.7	433	2 T04594	aldehyde dehydroge
100	30	85.7	441	2 AE2976	agaE protein (limp
101	30	85.7	441	2 F98306	agaE protein (limp
102	30	85.7	448	2 D86368	hypothetical prote

103	30	85.7	478	2	T15516	hypothetical prote	176	28	80.0	109	2	C82413	pterin-4-alpha-car
104	30	85.7	568	2	S28089	hypothetical prote	177	28	80.0	139	2	S41579	lysozyme (EC 3.2.1
105	30	85.7	612	2	T30438	tetratricopeptide-	178	28	80.0	148	2	C90369	hypothetical prote
106	30	85.7	719	2	T40403	exoglucanase - Clo	179	28	80.0	152	2	A97090	hypothetical prote
107	30	85.7	775	2	T07172	subtilisin-like pr	180	28	80.0	154	2	D82795	phage-related endo
108	30	85.7	843	1	H44001	env polyprotein pr	181	28	80.0	155	2	H83146	conserved hypochet
109	30	85.7	856	1	JC5256	adipocyte transcri	182	28	80.0	155	2	D87399	cytochrome c famil
110	30	85.7	856	1	A44963	env polyprotein pr	183	28	80.0	162	2	E86762	hypothetical prote
111	30	85.7	891	1	RDBEHP	nitrate reductase	184	28	80.0	192	2	H96828	hypothetical prote
112	30	85.7	904	1	RDNTNT	nitrate reductase	185	28	80.0	192	2	C89153	protein C24B5.4 [i
113	30	85.7	904	1	RDNTNS	nitrate reductase	186	28	80.0	192	2	C84033	hypothetical prote
114	30	85.7	909	2	JN0655	nitrate reductase	187	28	80.0	197	2	AB3212	2-hydroxychromene-
115	30	85.7	940	2	C84947	isoleucine-TRNA li	188	28	80.0	200	2	D97055	probable nucleotid
116	30	85.7	1494	2	C70152	serine/proteinase, k	189	28	80.0	200	2	D97224	probable GTPase, Y
117	30	85.7	2021	2	AD2267	sensory transducti	190	28	80.0	201	2	T51665	myb-related transc
118	30	85.7	2140	2	F95074	metalloproteinase	191	28	80.0	223	2	C70524	hypothetical prote
119	30	85.7	2144	2	A97942	hypothetical prote	192	28	80.0	229	2	AH1525	ABC transporter, A
120	30	85.7	2528	2	T20719	probable membrane	193	28	80.0	274	2	D86300	hypothetical prote
121	30	85.7	4910	2	S64942	hypothetical prote	194	28	80.0	280	2	C86889	zinc ABC transport
122	29	82.9	130	2	T04048	hypothetical prote	195	28	80.0	281	2	H64125	modD protein homol
123	29	82.9	142	2	T51902	hypothetical prote	196	28	80.0	281	2	T52189	ethylene responsiv
124	29	82.9	154	2	C87571	hypothetical prote	197	28	80.0	283	2	C88469	protein C28H8.7 [i
125	29	82.9	182	2	E87289	conserved hypochet	198	28	80.0	291	2	AE1828	hypothetical prote
126	29	82.9	255	2	AD1257	B. subtilis Reco p	199	28	80.0	325	2	T18283	conserved hypochet
127	29	82.9	259	2	C95849	conserved hypochet	200	28	80.0	329	2	G82243	hypothetical prote
128	29	82.9	260	2	T22792	hypothetical prote	201	28	80.0	332	2	T24725	probable exported
129	29	82.9	261	2	S52609	hypothetical prote	202	28	80.0	362	2	A10370	DNA repair and gen
130	29	82.9	275	2	B75479	conserved hypochet	203	28	80.0	370	1	D22930	translation releas
131	29	82.9	283	2	S06182	repressor protein	204	28	80.0	372	1	S76448	site-specific DNA-
132	29	82.9	283	2	S06182	transcriptional regu	205	28	80.0	377	1	S01615	hypothetical prote
133	29	82.9	284	2	AC2944	probable transcrip	206	28	80.0	379	2	B07777	ABC transporter, m
134	29	82.9	285	2	G72414	probable polynucle	207	28	80.0	405	2	A10006	DNA/pantothenate m
135	29	82.9	287	2	G98338	hypothetical prote	208	28	80.0	407	2	AC0971	conserved hypochet
136	29	82.9	295	2	D83587	hypothetical prote	209	28	80.0	407	2	T24273	hypothetical prote
137	29	82.9	311	2	D85631	ABC transporter, p	210	28	80.0	430	1	A65165	pantothenate metab
138	29	82.9	326	2	F81714	probable pdhA prot	211	28	80.0	430	2	B91193	pantothenate metab
139	29	82.9	348	2	T17304	hypothetical prote	212	28	80.0	430	2	C86040	protein T01B7.5 [i
140	29	82.9	367	2	A70550	conserved hypochet	213	28	80.0	445	2	H88244	fodrin alpha chain
141	29	82.9	379	2	G82402	hypothetical prote	214	28	80.0	454	2	S01092	hypothetical prote
142	29	82.9	388	2	H85692	probable host spec	215	28	80.0	457	2	E86080	chemotaxis protein
143	29	82.9	391	2	C90908	probable host spec	216	28	80.0	457	2	E91233	two-component sens
144	29	82.9	391	2	H90968	probable host spec	217	28	80.0	457	2	S40855	protein F46F5.7 [i
145	29	82.9	391	2	H90996	argininosuccinate	218	28	80.0	457	2	AD0943	hypothetical prote
146	29	82.9	401	2	G82737	hypothetical prote	219	28	80.0	465	2	H88029	gag polyprotein -
147	29	82.9	470	2	B96741	probable iron-sulf	220	28	80.0	476	2	T29463	cation ABC transpo
148	29	82.9	492	2	T36429	coat protein - car	221	28	80.0	478	1	FOVMVL	gag polyprotein -
149	29	82.9	494	1	VCCVCE	hypothetical prote	222	28	80.0	490	2	H69858	gag polyprotein -
150	29	82.9	651	2	F89798	conserved hypochet	223	28	80.0	500	1	FOVWL	hypothetical prote
151	29	82.9	671	2	B75607	phospholipase D (E	224	28	80.0	500	1	FOVWL	gag polyprotein -
152	29	82.9	808	2	T04092	phospholipase D (E	225	28	80.0	502	2	T19708	hypothetical prote
153	29	82.9	809	2	T11695	phospholipase D (E	226	28	80.0	506	1	A38068	gag polyprotein -
154	29	82.9	812	2	T03659	nitrate reductase	227	28	80.0	512	1	FOVWH3	gag polyprotein -
155	29	82.9	890	2	T11805	nitrate reductase	228	28	80.0	512	1	FOVWH3	probable membrane
156	29	82.9	898	1	RDBJNH	nitrate reductase	229	28	80.0	533	2	D83014	conserved hypochet
157	29	82.9	900	2	A95340	cation transport P	230	28	80.0	533	2	D83014	hypothetical prote
158	29	82.9	900	2	A95340	nitrate reductase	231	28	80.0	535	2	T23419	formylmethanofuran
159	29	82.9	911	1	RDTONH	nitrate reductase	232	28	80.0	535	2	G69074	formylmethanofuran
160	29	82.9	918	2	A41667	nitrate reductase	233	28	80.0	569	2	S57456	succinate dehydrog
161	29	82.9	920	2	S52301	hypothetical prote	234	28	80.0	571	2	C70353	hypothetical prote
162	29	82.9	977	2	D85741	host specificity p	235	28	80.0	603	2	E71444	probable EREBP-4 -
163	29	82.9	1132	1	QS8PL	host specificity p	236	28	80.0	603	2	JH0593	Schwann cell myeli
164	29	82.9	1132	2	H90834	probable host spec	237	28	80.0	623	2	A70741	hypothetical prote
165	29	82.9	1137	2	B90734	probable tail comp	238	28	80.0	623	2	T16384	hypothetical prote
166	29	82.9	1138	2	D85584	hypothetical prote	239	28	80.0	660	2	C86877	hypothetical prote
167	29	82.9	1149	2	T20891	probable host spec	240	28	80.0	662	2	T47649	ABC transporter-li
168	29	82.9	1157	2	A90769	probable host spec	241	28	80.0	688	2	T23108	hypothetical prote
169	29	82.9	1158	2	F90854	probable tail comp	242	28	80.0	749	2	A99438	hypothetical prote
170	29	82.9	1158	2	G85718	probable host spec	243	28	80.0	762	2	G88436	protein T04A8.13 [
171	29	82.9	1159	2	A90899	hypothetical prote	244	28	80.0	765	2	AD3549	diguanilate cyclas
172	29	82.9	1159	2	G85916	probable host spec	245	28	80.0	791	2	T24435	hypothetical prote
173	29	82.9	1165	2	F90877	probable host spec	246	28	80.0	917	1	RDMUNH	nitrate reductase
174	29	82.9	1165	2	D85842	probable tail fibe	247	28	80.0	938	2	T51422	hypothetical prote
175	29	82.9	1337	2	T38949	hypothetical prote	248	28	80.0				

249	28	80.0	950	2	T28793	diacylglycerol kin	322	27	77.1	301	2	T20651	hypothetical prote
250	28	80.0	952	2	T28792	diacylglycerol kin	323	27	77.1	303	2	S77235	hypothetical prote
251	28	80.0	956	2	B71250	valine-tRNA ligase	324	27	77.1	306	2	B69992	ABC transporter (m
252	28	80.0	957	2	H69141	hypothetical prote	325	27	77.1	306	2	T06042	hypothetical prote
253	28	80.0	1004	2	A39611	probable GTP-bind	326	27	77.1	309	1	PAHU2A	phosphoprotein pho
254	28	80.0	1108	2	T35827	probable membrane	327	27	77.1	309	1	A27430	phosphoprotein pho
255	28	80.0	1252	2	A47213	beta-fodrin - huma	328	27	77.1	309	1	S10371	phosphoprotein pho
256	28	80.0	1272	2	T30248	fragile X mental r	329	27	77.1	309	1	PABBA1	phosphoprotein pho
257	28	80.0	1297	2	S25714	son-of-sevenless-2	330	27	77.1	309	1	PART2A	phosphoprotein pho
258	28	80.0	1323	1	RRWGS	RNA-directed RNA p	331	27	77.1	309	1	S20348	phosphoprotein pho
259	28	80.0	1333	2	A37488	Ras guanine nucleo	332	27	77.1	309	1	PAHU2B	phosphoprotein pho
260	28	80.0	1336	2	S25716	Ras guanine nucleo	333	27	77.1	309	1	PAHU2B	phosphoprotein pho
261	28	80.0	1407	1	T00558	probable ABC trans	334	27	77.1	309	1	PAB2B2	phosphoprotein pho
262	28	80.0	1408	2	T47671	P-glycoprotein-lik	335	27	77.1	309	1	PART2B	phosphoprotein pho
263	28	80.0	1436	2	JC5290	protein-tyrosine-p	336	27	77.1	309	1	JC4316	phosphoprotein pho
264	28	80.0	1442	2	S72441	protein-tyrosine-p	337	27	77.1	309	2	T17557	phosphoprotein pho
265	28	80.0	1495	2	E86428	probable ABC trans	338	27	77.1	320	1	A05023	cytochrome c-type
266	28	80.0	1707	2	S77908	hypothetical prote	339	27	77.1	323	2	R84423	hypothetical prote
267	28	80.0	1811	2	T00035	nonstructural poly	340	27	77.1	324	2	D72070	conserved hypoteth
268	28	80.0	2228	2	E97942	beta-galactosidase	341	27	77.1	324	2	B86555	Crz9 hypothetical
269	28	80.0	2233	2	B95075	beta-galactosidase	342	27	77.1	325	2	A28029	phosphoprotein pho
270	28	80.0	2364	1	A44159	spectrin beta-G ch	343	27	77.1	327	2	G83921	hypothetical prote
271	28	80.0	3603	1	D69681	peptide synthetase	344	27	77.1	335	2	T36304	probable anthranil
272	28	80.0	3712	1	YCCEVC	alpha-aminoadipyl-	345	27	77.1	336	2	B97190	hypothetical prote
273	27	77.1	53	2	C82776	hypothetical prote	346	27	77.1	336	2	B87475	DNA polymerase III
274	27	77.1	64	1	QABP22	restriction inhibi	347	27	77.1	339	2	S35068	hypothetical prote
275	27	77.1	65	2	S76998	hypothetical prote	348	27	77.1	342	2	B82418	L-allo-threonine a
276	27	77.1	66	1	QABPL	restriction inhibi	349	27	77.1	347	2	R84773	hypothetical prote
277	27	77.1	76	2	S10068	restriction inhibi	350	27	77.1	348	2	T08327	hypothetical prote
278	27	77.1	100	2	C72690	hypothetical prote	351	27	77.1	348	2	S44628	f22b7.1 protein -
279	27	77.1	102	2	F97004	probable transcrip	352	27	77.1	351	2	JQ2327	ALI protein - Indi
280	27	77.1	107	2	A81995	hypothetical prote	353	27	77.1	355	2	F83914	hypothetical prote
281	27	77.1	115	2	AF1366	transcription regu	354	27	77.1	359	2	A72317	alcohol dehydrogen
282	27	77.1	115	2	AG1735	transcription regu	355	27	77.1	364	2	H75466	lipopolyaaccharide
283	27	77.1	120	2	A80398	probable sigma 54	356	27	77.1	365	2	T20652	hypothetical prote
284	27	77.1	124	2	C57842	hypothetical prote	357	27	77.1	366	2	D75096	aspartate aminotra
285	27	77.1	125	2	F81234	conserved hypoteth	358	27	77.1	369	2	T24620	hypothetical prote
286	27	77.1	126	2	F82008	hypothetical prote	359	27	77.1	373	2	A96927	probable N6-adenin
287	27	77.1	131	2	B30900	probable minor tai	360	27	77.1	381	2	T40864	hypothetical prote
288	27	77.1	140	2	S41573	lysozyme (EC 3.2.1	361	27	77.1	381	2	B97182	acyl-protein synth
289	27	77.1	144	2	D83209	hypothetical prote	362	27	77.1	390	2	B47013	butanol dehydrogen
290	27	77.1	145	2	G84148	hypothetical prote	363	27	77.1	390	2	D97305	NAOH-dependent bu
291	27	77.1	146	2	D95092	conserved hypoteth	364	27	77.1	395	2	B90421	hypothetical prote
292	27	77.1	146	2	A37960	conserved hypoteth	365	27	77.1	395	2	B90459	FIXC protein homol
293	27	77.1	162	2	D84684	hypothetical prote	366	27	77.1	396	2	F84326	GTP-binding protei
294	27	77.1	163	1	BRAD21	early E1B 19K prot	367	27	77.1	399	2	A82351	DNA/pantothenate m
295	27	77.1	192	2	C64767	yail protein - Esc	368	27	77.1	400	2	G54104	pantothenate metab
296	27	77.1	192	2	E90683	hypothetical prote	369	27	77.1	402	2	T19390	hypothetical prote
297	27	77.1	192	2	A85534	hypothetical prote	370	27	77.1	408	2	H90222	GTP binding protei
298	27	77.1	192	2	G97754	hypothetical prote	371	27	77.1	409	2	D64216	hypothetical prote
299	27	77.1	195	2	AC2527	hypothetical prote	372	27	77.1	412	2	AB1000	type II secretion
300	27	77.1	197	2	B83485	probable transcrip	373	27	77.1	414	2	AG2407	site-specific DNA-
301	27	77.1	208	2	I64209	ribosomal protein	374	27	77.1	423	2	D96552	unknown protein, 7
302	27	77.1	214	2	H84981	hypothetical prote	375	27	77.1	427	2	G83764	diaminobutyric aci
303	27	77.1	230	2	AG0931	conserved hypoteth	376	27	77.1	431	2	S04020	hypothetical prote
304	27	77.1	233	2	T48179	hypothetical prote	377	27	77.1	437	2	T03878	hypothetical prote
305	27	77.1	236	2	B56281	7alpha-cephen-meth	378	27	77.1	441	2	S73996	MG148 homolog Vxps
306	27	77.1	236	2	E70028	conserved hypoteth	379	27	77.1	445	2	A47676	bacteriocin 28b -
307	27	77.1	237	2	T21376	hypothetical prote	380	27	77.1	449	2	A47676	env polypeptide D
308	27	77.1	240	2	E84390	hypothetical prote	381	27	77.1	454	2	B41621	glutamate synthase
309	27	77.1	243	2	A26599	clathrin light cha	382	27	77.1	471	2	G82083	probable magnesium
310	27	77.1	247	2	T32859	hypothetical prote	383	27	77.1	487	2	G75255	glutamate synthase
311	27	77.1	248	2	E82892	conserved hypoteth	384	27	77.1	493	2	AC1856	diaminobutyrate-py
312	27	77.1	255	2	T06587	acid phosphatase (385	27	77.1	498	2	T09436	gag polypeptide -
313	27	77.1	264	2	A54060	nicotinamide N-met	386	27	77.1	507	2	T46161	glucosyltransferas
314	27	77.1	268	2	A52363	inositol monophosp	387	27	77.1	513	1	A47436	1,25-dihydroxyvita
315	27	77.1	271	2	C47127	tetracenomycin C s	388	27	77.1	514	2	S60033	25-hydroxyvitamin
316	27	77.1	271	2	E83942	hypothetical prote	389	27	77.1	522	2	A45228	25-hydroxyvitamin
317	27	77.1	276	2	A81095	hypothetical prote	390	27	77.1	524	2	A46103	transmembrane glyc
318	27	77.1	278	2	A81458	hypothetical prote	391	27	77.1	532	2	A35149	ipah protein - Shi
319	27	77.1	281	2	T30596	hypothetical prote	392	27	77.1	537	2	C97765	CTP synthase (EC 6
320	27	77.1	290	2	A82687	conserved hypoteth	393	27	77.1	539	2	T38927	hypothetical prote
321	27	77.1	292	1	E64226	hypothetical prote	394	27	77.1	541	2	A82320	methyl-accepting c
										549	2	B86264	hypothetical prote

395	27	77.1	1066	2	T30903	arachidonate 8-lip
396	27	77.1	1139	2	S40932	hypothetical prote
397	27	77.1	1148	2	A28614	nonstructural poly
398	27	77.1	1159	2	T15963	hypothetical prote
399	27	77.1	1161	2	T59311	nardilysin (SC 3.4
400	27	77.1	1179	2	T04584	TMV resistance pro
401	27	77.1	1188	2	T20333	hypothetical prote
402	27	77.1	1188	2	T20333	E2 glycoprotein pr
403	27	77.1	1353	1	JQ2168	nuclear protein ST
404	27	77.1	1359	2	A49883	surface protein -
405	27	77.1	1361	2	S29998	surface glycoprote
406	27	77.1	1362	2	A37474	E2 glycoprotein pr
407	27	77.1	1363	1	VG1HNM	E2 glycoprotein pr
408	27	77.1	1363	1	VG1HQU	E2 glycoprotein pr
409	27	77.1	1363	1	VG1HFI	E2 glycoprotein pr
410	27	77.1	1363	1	VG1HL9	E2 glycoprotein pr
411	27	77.1	1363	1	VG1HVA	E2 glycoprotein pr
412	27	77.1	1363	1	VG1HLY	surface protein -
413	27	77.1	1363	1	S44240	surface protein -
414	27	77.1	1363	2	S44241	myosin-like protei
415	27	77.1	1374	2	D85390	myosin heavy chain
416	27	77.1	1375	2	S03200	DNA polymerase III
417	27	77.1	1443	2	S73446	hypothetical prote
418	27	77.1	1490	2	T20513	hypothetical prote
419	27	77.1	1490	2	T20513	hypothetical prote
420	27	77.1	1494	2	T28452	myosin MYAI, class
421	27	77.1	1520	2	S46444	probable membrane
422	27	77.1	1520	2	S46444	transcription acti
423	27	77.1	1559	1	S64757	probable transcrip
424	27	77.1	1638	2	A42091	hypothetical prote
425	27	77.1	1680	2	T17272	myosin heavy chain
426	27	77.1	1780	2	T17272	receptor tyrosine
427	27	77.1	1968	1	S05697	tiggrin - fruit fl
428	27	77.1	2051	2	T30938	hypothetical prote
429	27	77.1	2186	2	T13169	
430	27	77.1	2331	2	T25410	
431	27	77.1	2331	2	T25410	
432	27	77.1	2331	2	T25410	
433	27	77.1	2331	2	T25410	
434	27	77.1	2331	2	T25410	
435	27	77.1	2331	2	T25410	
436	27	77.1	2331	2	T25410	
437	27	77.1	2331	2	T25410	
438	27	77.1	2331	2	T25410	
439	27	77.1	2331	2	T25410	
440	27	77.1	2331	2	T25410	
441	27	77.1	2331	2	T25410	
442	27	77.1	2331	2	T25410	
443	27	77.1	2331	2	T25410	
444	27	77.1	2331	2	T25410	
445	27	77.1	2331	2	T25410	
446	27	77.1	2331	2	T25410	
447	27	77.1	2331	2	T25410	
448	27	77.1	2331	2	T25410	
449	27	77.1	2331	2	T25410	
450	27	77.1	2331	2	T25410	
451	27	77.1	2331	2	T25410	
452	27	77.1	2331	2	T25410	
453	27	77.1	2331	2	T25410	
454	27	77.1	2331	2	T25410	
455	27	77.1	2331	2	T25410	
456	27	77.1	2331	2	T25410	
457	27	77.1	2331	2	T25410	
458	27	77.1	2331	2	T25410	
459	27	77.1	2331	2	T25410	
460	27	77.1	2331	2	T25410	
461	27	77.1	2331	2	T25410	
462	27	77.1	2331	2	T25410	
463	27	77.1	2331	2	T25410	
464	27	77.1	2331	2	T25410	
465	27	77.1	2331	2	T25410	
466	27	77.1	2331	2	T25410	
467	27	77.1	2331	2	T25410	

ALIGNMENTS

RESULT 1

S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:G60179; PIDN:CAA43622.1; PID:G60180
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebra
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:G60179
C:Superfamily: type E retrovirus env polyprotein
Query Match 100.0%; Score 35; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 163 ELDKWA 168

RESULT 2

S21996
 A:Title: envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S70422; S21996
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by phylogenetic analysis
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70422
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A:Cross-references: EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:G1067129
 A:Experimental source: patient 27L
 A:Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 163 ELDKWA 168

RESULT 3

S21992
 A:Title: envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S70424; S21992
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by phylogenetic analysis
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70424
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <ST2>
 A:Cross-references: EMBL:X61358; NID:G60177; PIDN:CAA43628.1; PID:G60178
 A:Experimental source: patient 22
 A:Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 163 ELDKWA 168

RESULT 4

S21998
 A:Title: envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: isolate 28
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S21998; S70425
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 submitted to the EMBL Data Library, July 1991
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by phylogenetic analysis
 A:Reference number: S21990
 A:Accession: S21998
 A:Molecule type: DNA
 A:Residues: 1-358 <ST1>
 A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by phylogenetic analysis
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70425
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-222, 'X', 224-358 <ST2>
 A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183
 C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 358;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 164 ELDKWA 169

RESULT 5

C41621
 A:Title: env polyprotein P - human immunodeficiency virus type 1 (fragment)
 N:Alternate names: coat polyprotein
 N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C>Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
 C:Accession: C41621
 R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
 A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A:Reference number: A41621; MUID:92107924; PMID:1763038
 A:Accession: C41621
 A:Molecule type: DNA
 A:Residues: 1-443
 A:Cross-references: GB:M77230; NID:G328631; PIDN:AAB03792.1; PID:G555015
 A:Note: this virus was isolated from the mother's sexual partner
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polyprotein
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
 F:424-443/Domain: transmembrane #status predicted <TMN>
 F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,377/Binding site: ca

Query Match 100.0%; Score 35; DB 2; Length 443;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 402 ELDKWA 407

RESULT 6

A41621
 A:Title: env polyprotein M - human immunodeficiency virus type 1 (fragment)
 N:Alternate names: coat polyprotein
 N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Note: host Homo sapiens (man)
 C>Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
 C:Accession: A41621
 R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
 A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
 A:Reference number: A41621; MUID:92107924; PMID:1763038
 A:Accession: A41621
 A:Molecule type: DNA
 A:Residues: 1-445
 A:Cross-references: GB:M77228; NID:G328627; PIDN:AAB03790.1; PID:G555013
 A:Note: this virus was isolated from the mother
 C:Genetics:

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A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F;1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>
F;254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>
F;426-445/Domain: transmembrane #status predicted <TM>
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:
F;9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 100.0%; Score 35; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
Db 404 ELDKWA 409

RESULT 7
S59898
kynureninase (EC 3.7.1.3) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S59898
R;Takeuchi, F.; Tsubouchi, R.; Yoshino, M.; Shibata, Y.
Biochim. Biophys. Acta 1252, 185-188, 1995
A;Title: Amino-acid sequence of rat liver kynureninase.
A;Reference number: S59898; MUID:96049498; PMID:7578221
A;Accession: S59898
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-464 <TA>
C;Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
Db 90 ELDKWA 95

RESULT 8
T48675
kynureninase (EC 3.7.1.3) [validated] - rat
N;Alternate names: L-kynurenine hydrolase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
C;Accession: T48675
R;Toma, S.; Nakamura, M.; Tone, S.; Okuno, E.; Kido, R.; Breton, J.; Avanzi, N.; Cozzi, F.
FEBS Lett. 408, 5-10, 1997
A;Title: Cloning and recombinant expression of rat and human kynureninase.
A;Reference number: Z24527; MUID:97324088; PMID:9180257
A;Accession: T48675
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-464 <TOM>
A;Cross-references: EMBL:U68168; NID:g1532215; PIDN:AAC53206.1; PID:g1532215
A;Experimental source: liver
C;Function:
A;Description: EC 3.7.1.3 [validated, MUID:97324088]
A;Pathway: biosynthesis of NAD cofactors
C;Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
Db 90 ELDKWA 95

RESULT 9
G02652
kynureninase (EC 3.7.1.3) - human
N;Alternate names: L-kynurenine hydrolase
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02652
R;Waltherbe, P.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01539
A;Accession: G02652
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-465 <MAL>
A;Cross-references: EMBL:U57721; NID:g1323714; PIDN:AAC50650.1; PID:g1323715
C;Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
Db 90 ELDKWA 95

RESULT 10
T16409
hypothetical protein F48E8.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16409
R;Kirsten, J.
submitted to the EMBL Data Library, March 1995
A;Description: The sequence of C. elegans cosmid F48E8.
A;Reference number: S59413
A;Accession: T16409
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-817 <KIR>
A;Cross-references: EMBL:U23514; NID:g746484; PID:g746490; PIDN:AAC46543.1; CESP:F48E8.6
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F48E8.6
A;Introns: 107/3; 510/3; 670/3; 733/3

Query Match 100.0%; Score 35; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
Db 359 ELDKWA 364

RESULT 11
VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N;Alternate names: coat polyprotein
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: JQ0066
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunodeficiency virus type 1.
A;Reference number: JQ0065; MUID:90034200; PMID:2806917
A;Accession: JQ0066
A;Molecule type: DNA
A;Residues: 1-846 <SPI>
A;Cross-references: GB:M27323; NID:g328154; PIDN:AAA44873.1; PID:g328162
A;Note: the authors translated the codon GCG for residue 523 as Arg


```
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match      100.0%; Score 35; DB 1; Length 846;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      652 ELDKWA 657

RESULT 12
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C;Accession: T09448
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A;Reference number: Z16673
A;Accession: T09448
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-847 <PAN>
A;Cross-references: EMBL:U63632; NID:gl465777; PID:gl465781
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein

Query Match      100.0%; Score 35; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      653 ELDKWA 658

RESULT 13
S13289
env protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S13289
R;O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A;Reference number: S13288; MUID:91043044; PMID:2172833
A;Accession: S13289
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-847 <ORR>
C;Superfamily: type E retrovirus env polyprotein

Query Match      100.0%; Score 35; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      653 ELDKWA 658

RESULT 14
```

```
S33985
env polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C;Accession: S33985
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33985
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-851 <CAR>
A;Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C;Superfamily: type E retrovirus env polyprotein

Query Match      100.0%; Score 35; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      657 ELDKWA 662

RESULT 15
VCLJBR
env polyprotein - human immunodeficiency virus type 1 (isolate BR)
N;Alternate names: coat polyprotein
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997
C;Accession: A31667
R;Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.
Virology 168, 79-89, 1989
A;Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)
A;Reference number: A94389; MUID:89085613; PMID:2789516
A;Accession: A31667
A;Molecule type: DNA
A;Residues: 1-852 <ANA>
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F:1-516/Product: coat protein gp120 #status predicted <CP1>
F:517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match      100.0%; Score 35; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      658 ELDKWA 663

RESULT 16
T12016
envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T12016
R;McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A;Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
A;Reference number: Z17379; MUID:98178716; PMID:9519894
A;Accession: T12016
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-852 <MCC>
A;Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
C;Genetics:
A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
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Thu Mar 18 10:20:34 2004

Query Match 100.0%; Score 35; DB 2; Length 852;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 658 ELDKWA 663

RESULT 17
S54384
envelope polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
C:Accession: S54384
R:Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <THE>
A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 100.0%; Score 35; DB 2; Length 853;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 659 ELDKWA 664

RESULT 18
S13288
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 660 ELDKWA 665

RESULT 19
VCLJ22
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03976
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh
Science 227, 484-492, 1985
A:title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A:Reference number: A04003; MUID:85090453; PMID:2578227
A:Accession: A03976

A:Molecule type: DNA
A:Residues: 1-855 <SAN>
A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666
C:Genetics:
A:Gene: env
A:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: exterior membrane glycoprotein #status predicted <TMM>
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 661 ELDKWA 666

RESULT 20
VCLJ2R
env polyprotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: D26192
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti
A:Reference number: A26192; MUID:87248097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SRI>
A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polyprotein #status predicted <MAT>
F:20-850/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TMM>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 100.0%; Score 35; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 661 ELDKWA 666

RESULT 21
VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dor
nberger, J.A.; Papas, T.S.; Graybe, J.; Chang, N.I.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA44,

C;Genetics: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
 F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
 F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
 F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 856;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 662 ELDKWA 667

RESULT 22
 VCLJVL
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
 N;Alternate names: coat polyprotein
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
 C;Accession: A03974
 R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laaky, L.A.; Capon, D.J.
 Nature 313, 450-458, 1985
 A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus
 A;Reference number: A93355; MUID:8511157; PMID:2982104
 A;Accession: A03974
 A;Molecule type: DNA
 A;Residues: 1-856 <MUE>
 A;Cross-references: GB:K02083; NID:g555008; PIDN:AB59873.1; PID:g328559
 C;Genetics: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
 F;512-856/Product: transmembrane glycoprotein #status predicted <TM>
 F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
 F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 35; DB 1; Length 856;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 662 ELDKWA 667

RESULT 23
 VCLJ3W
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
 N;Contains: coat protein gp120; coat protein gp41
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
 C;Accession: A24774
 R;Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
 Cell 45, 637-648, 1986
 A;Title: Identification and characterization of conserved and variable regions in the env
 A;Reference number: A24774; MUID:86218077; PMID:2423250
 A;Accession: A24774
 A;Molecule type: DNA
 A;Residues: 1-856 <STA>
 A;Cross-references: GB:K03455; GB:M38432; NID:g1906382
 C;Genetics: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-501/Product: coat protein gp120 #status predicted <GP1>
 F;502-847/Product: coat protein gp41 #status predicted <GP2>
 F;87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 100.0%; Score 35; DB 1; Length 856;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 662 ELDKWA 667

RESULT 24
 VCLJWN
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)
 N;Alternate names: coat polyprotein
 C;Species: human immunodeficiency virus type 1, HIV-1
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
 C;Accession: A28922
 R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Colialti, E.; Farrell, K.; Wong-Sta
 virology 164, 531-536, 1988
 A;Title: Envelope sequences of two new United States HIV-1 isolates.
 A;Reference number: A28922; MUID:88219542; PMID:3369091
 A;Accession: A28922
 A;Molecule type: DNA
 A;Residues: 1-859 <GUR>
 C;Genetics: env
 C;Superfamily: type E retrovirus env polyprotein
 C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-859/Product: env polyprotein #status predicted <PPP>
 F;87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 100.0%; Score 35; DB 1; Length 859;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 666 ELDKWA 671

RESULT 25
 T01672
 envelope polyprotein precursor - human immunodeficiency virus type 1
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
 C;Accession: T01672
 R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
 Cell 46, 63-74, 1986
 A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
 A;Reference number: Z14389; MUID:86245056; PMID:2424612
 A;Accession: T01672
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-859 <ALI>
 A;Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234
 C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 859;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 664 ELDKWA 669

RESULT 26

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC F4118 genomic sequence.
A;Reference number: 214674
A;Accession: T02448
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-268 <ROU>
A;Cross-references: EMBL:AC004665; NID:g3386593; PID:g3386596
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.V.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Unayam, L.; Tallon, J.;
Cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.B.; Fraser, C.M.; Venter, L.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84897
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 <STO>
A;Cross-references: GB:AR002093; NID:g3702346; PIDN:AAC62903.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g45990; F4118.3
A;Map position: 2
A;Introns: 267/3; 53/3; 83/3; 139/2; 162/3; 189/2; 210/2; 236/1
Query Match 91.4%; Score 32; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 227 ELDKWS 232
RESULT 30
E71561
probable solute protein binding - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2000
C;Accession: E71561
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marache, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: E71561
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-326 <ARN>
A;Cross-references: GB:AR001281; GB:AR001273; NID:g3328454; PIDN:AAC67658.1; PID:g332846
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: YtgA
C;Superfamily: adhesin B
Query Match 91.4%; Score 32; DB 2; Length 326;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 184 ELDRWA 189
RESULT 31
D71274
probable prolipoprotein diacylglycerol transferase (lgt) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 15-Sep-2000
C;Accession: D71274
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: D71274
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-332 <COL>
A;Cross-references: GB:AE001255; GB:AE000520; NID:g3323156; PIDN:AAC65817.1; PID:g332316
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0852
C;Superfamily: prolipoprotein diacylglycerol transferase
Query Match 91.4%; Score 32; DB 2; Length 332;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 47 ELDKWS 52
RESULT 32
C83347
probable dipeptidase precursor PA2393 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83347
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83347
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <STO>
A;Cross-references: GB:AE004665; GB:AE004091; NID:g9948426; PIDN:AAG05781.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2393
Query Match 91.4%; Score 32; DB 2; Length 448;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 180 QLDKWA 185
RESULT 33
S51160
nitrate reductase (NADH) (EC 1.7.1.1) (clone Znmrls) - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 03-Jun-2002
C;Accession: S51160
R;Campbell, W.H.
submitted to the EMBL Data Library, May 1994
A;Description: Expression in Escherichia coli of cytochrome c reductase activity from a
A;Reference number: S51160
A;Accession: S51160
A;Molecule type: mRNA
A;Residues: 1-501 <CAM>
A;Cross-references: EMBL:M77792; NID:g168516; PIDN:AAA33483.1; PID:g168517
A;Experimental source: strain W64xW182E; scutellum
C;Genetics:
A;Gene: nar-15
C;Complex: homodimer
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 redu
C;Keywords: dimer; electron transfer; FAD; flavoprotein; heme; iron; metalloprotein; mol
F;1-67/Domain: molybdopterin-binding domain homology (fragment) <PCO>

F;129-203/Domain: cytochrome b5 core homology <CB5>
F;248-501/Domain: cytochrome-b5 reductase homology <CBR>
F;164,187/Binding site: heme iron (His) (axial ligands) #status predicted

Query Match 91.4%; Score 32; DB 2; Length 501;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||:|
Db 417 ELDRWA 422

RESULT 34
S19254
nitrate reductase (NADH) (EC 1.7.1.1) flavin chain (clone Zmr1) - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 03-Jun-2002
C;Accession: S19254; S58710; A35499
R;Gowri, G.; Campbell, W.H., 1989
Plant Physiol. 90, 792-798, 1989
A;Title: cDNA clones for corn leaf NADH: nitrate reductase and chloroplast NAD(P) (+): g
A;Reference number: S19254
A;Accession: S19254
A;Molecule type: mRNA
A;Residues: 1-617 <GOW>
A;Cross-references: EMBL:M27821
A;Accession: S58710
A;Molecule type: protein
A;Residues: 'RII', '369', 'TPA', '373', 'SDNYHFKELAVRAD', '390', 'S', '392', 'NTHLETAATAAPG', '406', 'K', '4
R;Hyde, G.E.; Campbell, W.H.
Biochem. Biophys. Res. Commun. 169, 1285-1291, 1990
A;Title: High-level expression in Escherichia coli of the catalytically active flavin d
A;Reference number: A35499; MUID:90267474; PMID:2189408
A;Accession: A35499
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 364-388, 'DQ', '391-404', 'SI', '407-413', 'AY', '415', 'P', '417-617 <HYD>
A;Cross-references: GB:M27821
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
C;Keywords: dimer; electron transfer; FAD; flavoprotein; heme; iron; metalloprotein; mol
F;1-187/Domain: molybdopter-in-binding domain homology (fragment) <PCO>
F;249-323/Domain: cytochrome b5 core homology <CB5>
F;368-617/Domain: cytochrome-b5 reductase homology <CBR>
F;284,307/Binding site: heme iron (His) (axial ligands)
F;431,589/Binding site: NAD (Lys, Cys) #status predicted
F;471/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 2; Length 617;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||:|
Db 536 ELDRWA 541

RESULT 35
VCLJH4
env polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
N;Alternate names: coat polyprotein
N;Contains: coat protein gp120; coat protein gp41
C;Species: human immunodeficiency virus type 1 HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: C25523
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
A;Reference number: A94136; MUID:87041461; PMID:3490666
A;Accession: C25523
A;Molecule type: DNA
A;Residues: 1-868 <DES>
A;Cross-references: GB:M13137; NID:G326460; PIDN:AAA44311.1; PID:G326467

C;Genetics:

A;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote:
F;1-521/Product: coat protein gp120 #status predicted <GP1>
F;522-868/Product: coat protein gp41 #status predicted <GP2>
F;89,138,139,142,166,195,198,208,245,252,273,287,300,312,342,349,365,371,395,405,409,459,
Query Match 91.4%; Score 32; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
:|||||
Db 674 QLDKWA 679

RESULT 36
T02240
nitrate reductase [NAD(P)H] (EC 1.7.1.2) - maize
C;Species: Zea mays (maize)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 03-Jun-2002
C;Accession: T02240
R;Campbell, W.H.; Redinbaugh, M.G.; Ingemarsson, B.; Dougherty, E.S.; Campbell, E.R.
submitted to the EMBL Data Library, January 1995
A;Description: A third nitrate reductase gene is expressed in corn tissues and suspensio
A;Reference number: Z14635
A;Accession: T02240
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-889 <CAM>
A;Cross-references: EMBL:U20450; NID:G676849; PIDN:AAA62316.1; PID:G676850
A;Experimental source: strain B73; seedling
C;Genetics:
A;Insertions: 336/1; 383/1; 460/3
C;Function:
A;Description: catalyzes the reduction of nitrate to nitrite using NAD(P)H as the electr
A;Pathway: nitrate assimilation
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 red
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; molybdenum; mol
F;82-459/Domain: molybdopter-in-binding domain homology <PCO>
F;520-594/Domain: cytochrome b5 core homology <CB5>
F;637-889/Domain: cytochrome-b5 reductase homology <CBR>
F;181/Binding site: molybdopter-in (Cys) (covalent) #status predicted
F;420/Disulfide bonds: interchain #status predicted
F;555,578/Binding site: heme iron (His) (axial ligands) #status predicted
F;701,861/Binding site: NAD(P) (Lys, Cys) #status predicted
F;741/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 2; Length 889;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||:|
Db 806 ELDRWA 811

RESULT 37
RDBHNS
nitrate reductase (NADH) (EC 1.7.1.1) - barley (cv. Steptoe) (fragment)
C;Species: Hordeum vulgare (barley)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002
C;Accession: S17454
R;Schnorr, K.M.; Juricek, M.; Huang, C.; Culley, D.; Kleinhofs, A.
Mol. Gen. Genet. 227, 411-416, 1991
A;Title: Analysis of barley nitrate reductase cDNA and genomic clones.
A;Reference number: S17453; MUID:91326031; PMID:1865878
A;Accession: S17454
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-912 <SCH>
A;Cross-references: EMBL:X57844; NID:gl9044; PIDN:CAA40975.1; PID:gl9045

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1991
C;Genetics:
A;Map position: 6
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
F;82-474/Domain: molybdopterin-binding domain homology <PCO>
F;535-609/Domain: cytochrome b5 core homology <CB5>
F;658-912/Domain: cytochrome-b5 reductase homology <CBR>
F;186/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;425/Disulfide bonds: interchain #status predicted
F;570,593/Binding site: heme iron (His) (axial ligands) #status predicted
F;722,894/Binding site: NAD (Lys, Cys) #status predicted
F;763/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 1; Length 912;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||:|
Db 828 ELDRWA 833

RESULT 38
RDBNH
nitrate reductase (NADH) (EC 1.7.1.1) - barley (cv. Himalaya)
C;Species: Hordeum vulgare (barley)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002
C;Accession: S17453
R;Schnorr, K.M.; Juricek, M.; Huang, C.; Culley, D.; Kleinhofs, A.
Mol. Gen. Genet. 227, 411-416, 1991
A;Title: Analysis of barley nitrate reductase cDNA and genomic clones.
A;Reference number: S17453; MUID:91326031; PMID:1865878
A;Accession: S17453
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-915 <SCH>
A;Cross-references: EMBL:X57845; NID:gl8993; PIDN:CAA40976.1; PID:gl8994
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1991
C;Genetics:
A;Map position: 6
A;Introns: 391/1
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
F;85-477/Domain: molybdopterin-binding domain homology <PCO>
F;538-612/Domain: cytochrome b5 core homology <CB5>
F;661-915/Domain: cytochrome-b5 reductase homology <CBR>
F;189/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;428/Disulfide bonds: interchain #status predicted
F;573,596/Binding site: heme iron (His) (axial ligands) #status predicted
F;725,887/Binding site: NAD (Lys, Cys) #status predicted
F;766/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 1; Length 915;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||:|
Db 831 ELDRWA 836

RESULT 39
S07554
nitrate reductase (NADH) (EC 1.7.1.1) - rice
C;Species: Oryza sativa (rice)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Jun-2002
C;Accession: S07554
R;Choi, H.K.; Kleinhofs, A.; An, G.
Plant Mol. Biol. 13, 731-733, 1989
A;Title: Nucleotide sequence of rice nitrate reductase genes.
A;Reference number: S07554; MUID:91370859; PMID:2491689
A;Accession: S07554

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-916 <CHO>
A;Cross-references: EMBL:X15819
C;Genetics:
A;Gene: nial
A;Introns: 347/1; 394/1; 471/3
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase
C;Keywords: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron;
F;88-480/Domain: molybdopterin-binding domain homology <PCO>
F;541-615/Domain: cytochrome b5 core homology <CB5>
F;663-916/Domain: cytochrome-b5 reductase homology <CBR>
F;192/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;431/Disulfide bonds: interchain #status predicted
F;576,599/Binding site: heme iron (His) (axial ligands) #status predicted
F;727,888/Binding site: NAD(P) (Lys, Cys) #status predicted
F;767/Binding site: FAD (Tyr) #status predicted

Query Match 91.4%; Score 32; DB 2; Length 916;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||:|
Db 832 ELDRWA 837

RESULT 40
S77910
hypothetical protein 1 - grapevine virus A
C;Species: Grapevine virus A
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C;Accession: S77910
R;Minafra, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: S77910
A;Accession: S77910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1707 <MIN>
A;Cross-references: EMBL:X75433; NID:gl405614; PIDN:CAA53182.1; PID:gl405615
C;Superfamily: grapevine trichovirus B hypothetical protein

Query Match 91.4%; Score 32; DB 2; Length 1707;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
:||||
Db 1457 DLDKWA 1462

RESULT 41
E82798
hypothetical protein XF0509 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82798
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82798
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-78 <SIN>
A;Cross-references: GB:AE003899; GB:AE003849; NID:G9105351; PIDN:AAF83319.1; GSPDB:GN001
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigz chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshukano, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328
A;Contents: annotation
A;Genetics:
A;Gene: XF0509

Query Match 88.6%; Score 31; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
DB 42 ELDKW 46

RESULT 42
C64746
yafu protein - Escherichia coli (strain K-12)
N;Alternate names: hypothetical protein b0218
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: C64746
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64746
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-112 <BLAT>
A;Cross-references: GB:AE000130; GB:U00096; NID:g1786402; PIDN:AACT3322.1; PID:g1786411; A;Experimental source: strain K-12, substrain MGL655
C;Genetics:
A;Gene: yafu
C;Superfamily: Escherichia coli yafu protein

Query Match 88.6%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
DB 90 ELDKW 94

RESULT 43
H70387
hypothetical protein aq_1018 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jun-2000
C;Accession: H70387
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196866; PMID:9537320
A;Accession: H70387
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-126 <AQF>
A;Cross-references: GB:AE000718; NID:g2983504; PIDN:AACT07091.1; PID:g2983514; GB:AE00069 A;Experimental source: strain VFS
C;Genetics:
A;Gene: aq_1018
C;Superfamily: Aquifex aeolicus hypothetical protein aq_1018

Query Match 88.6%; Score 31; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
DB 95 ELDKW 99

RESULT 44
AB0550
conserved hypothetical protein STY0420 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0550
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08842.1; PID:g16501656; GSPDB:GN00176 C;Genetics:
A;Gene: STY0420
C;Superfamily: yaiI protein

Query Match 88.6%; Score 31; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
DB 139 ELDKW 143

RESULT 45
AH0368
conserved hypothetical protein YPO3033 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AH0368
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92275.1; PID:g15980986; GSPDB:GN00175 C;Genetics:
A;Gene: YPO3033
C;Superfamily: yaiI protein

Query Match 88.6%; Score 31; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
|||||
DB 139 ELDKW 143

RESULT 46

A45332
zipper protein - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C:Accession: A45332
R:Bikle, D.D.; Munson, S.; Morrison, N.; Eisman, J.
J. Biol. Chem. 268, 620-626, 1993
A:Title: Zipper protein, a newly described tropomyosin-like protein of the intestinal brush border.
A:Reference number: A45332; MUID:93107070; PMID:7678004
A:Accession: A45332
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-201 <BIK>
A:Experimental source: intestine
A:Note: sequence extracted from NCBI backbone (NCBIP:121450)

Query Match 88.6%; Score 31; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
|||||
Db 62 ELDKW 66

RESULT 47
AF1167
ABC transporter, ATP-binding protein homolog lmo0742 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF1167
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1167
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-229 <GLA>
A:Cross-references: GB:NC 003210; PIDN:CAC98920.1; PID:g16410131; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0742

Query Match 88.6%; Score 31; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
|||||
Db 104 ELDKW 108

RESULT 48
B83030
probable rRNA methylase PA4936 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83030
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: B83030
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <STO>

A:Cross-references: GB:AE004906; GB:AE004091; NID:9951206; PIDN:AAG08321.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4936
C:Superfamily: conserved hypothetical protein HI0860

Query Match 88.6%; Score 31; DB 2; Length 248;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
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Db 59 ELDEWA 64

RESULT 49
T33683
hypothetical protein T12B5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C:Accession: T33683
R:Langston, Y.; Wohldmann, P.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid T12B5.
A:Reference number: Z21387
A:Accession: T33683
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-338 <LAN>
A:Cross-references: EMBL:AF100307; PIDN:AAC68928.1; GSPDB:GN000021; CESP:T12B5.2
A:Experimental source: strain Bristol N2; clone T12B5
C:Genetics:
A:Gene: CESP:T12B5.2
A:Map position: 3
A:Introns: 34/2; 62/2; 269/3
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

Query Match 88.6%; Score 31; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
|||||
Db 19 ELDKW 23

RESULT 50
T20280
hypothetical protein cTel54X.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C:Accession: T20280
R:Smeye, R.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z19248
A:Accession: T20280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-343 <WIL>
A:Cross-references: EMBL:AL031226; PIDN:CAA20224.1; GSPDB:GN000021; CESP:cTel54X.1
C:Genetics:
A:Gene: CESP:cTel54X.1
A:Map position: 3
A:Introns: 34/2; 62/2; 265/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C29F9.11

Query Match 88.6%; Score 31; DB 2; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
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Db 19 ELDKW 23

Search completed: March 16, 2004, 09:18:20
Job time : 31 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2004, 09:09:50 ; Search time 11 Seconds
(without alignments)
28.402 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	464	1 KYNH_RAT	P70712 rattus norv
2	35	100.0	465	1 KYNH_HUMAN	Q16719 homo sapien
3	35	100.0	817	1 YR86_CABEL	Q09568 caenorhabdi
4	35	100.0	846	1 ENV_HV1ND	P18799 human immun
5	35	100.0	847	1 ENV_HV1S1	P19550 human immun
6	35	100.0	847	1 ENV_HV1W2	P05880 human immun
7	35	100.0	848	1 ENV_HV1JR	P20871 human immun
8	35	100.0	851	1 ENV_HV1B8	P04582 human immun
9	35	100.0	852	1 ENV_HV1BN	P12488 human immun
10	35	100.0	852	1 ENV_HV1S3	P19549 human immun
11	35	100.0	853	1 ENV_HV1EL	P04581 human immun
12	35	100.0	853	1 ENV_HV1MP	P19551 human immun
13	35	100.0	853	1 ENV_HV1Z2	P12487 human immun
14	35	100.0	855	1 ENV_HV1A2	P03378 human immun
15	35	100.0	855	1 ENV_HV1OY	P20888 human immun
16	35	100.0	855	1 ENV_HV1Z6	P04580 human immun
17	35	100.0	856	1 ENV_HV1B1	P03375 human immun
18	35	100.0	856	1 ENV_HV1H2	P04578 human immun
19	35	100.0	856	1 ENV_HV1H3	P04624 human immun
20	35	100.0	856	1 ENV_HV1LW	Q70626 human immun
21	35	100.0	856	1 ENV_HV1MN	P05877 human immun
22	35	100.0	856	1 ENV_HV1PV	P03376 human immun
23	35	100.0	856	1 ENV_HV1SC	P05878 human immun
24	35	100.0	856	1 ENV_HV1W1	P11872 human immun
25	35	100.0	859	1 ENV_HV1MA	P04583 human immun
26	35	100.0	861	1 ENV_HV1BR	P03377 human immun
27	35	100.0	865	1 ENV_HV1RH	P04579 human immun
28	35	100.0	926	1 NIA_SPIOL	P23312 spinacia ol
29	32	91.4	326	1 Y067_CHLTR	Q98529 chlamydia t
30	32	91.4	332	1 LGT_TREP	O83824 treponema p
31	32	91.4	358	1 T2S1_STRAH	O31074 streptomyce
32	32	91.4	621	1 NIA1_MAIZE	P17571 zea mays (m
33	32	91.4	863	1 ENV_HV1Z8	P05882 human immun

34	32	91.4	868	1 ENV_HV1C4	P05879 human immun
35	32	91.4	889	1 NIA3_MAIZE	P49102 zea mays (m
36	32	91.4	912	1 NIA2_HORVU	P27969 hordeum vul
37	32	91.4	915	1 NIA1_HORVU	P27967 hordeum vul
38	32	91.4	916	1 NIA1_ORYZA	P16081 oryza sativ
39	32	91.4	1073	1 ACA9_ARATH	P16081 oryza sativ
40	31	88.6	112	1 YAFU_ECOLI	P77354 escherichia
41	31	88.6	151	1 YAI1_SALTY	Q8xemi salmonella
42	31	88.6	152	1 YU33_YERPE	Q8zcf8 yersinia pe
43	31	88.6	381	1 DHB2_MOUSE	P51658 mus musculu
44	31	88.6	388	1 GAG_HV1W2	P05889 human immun
45	31	88.6	392	1 GAL1_STRPN	Q07n26 streptococc
46	31	88.6	392	1 GAL1_STRR6	Q8dnk7 streptococc
47	31	88.6	421	1 ECB2_HALEL	O52250 halomonas e
48	31	88.6	498	1 GAG_HV1OY	P20889 human immun
49	31	88.6	499	1 GAG_HV1N5	P12493 human immun
50	31	88.6	499	1 GAG_HV1Y2	P35962 human immun
51	31	88.6	501	1 GAG_HV1A2	P03349 human immun
52	31	88.6	785	1 APE3_SULSO	P95928 sulfolobus
53	31	88.6	854	1 ENV_SIVCZ	P17281 chimpanzee
54	31	88.6	880	1 SYV_BACST	P11931 bacillus st
55	31	88.6	881	1 NIA1_PHAVU	P39865 phaseolus v
56	31	88.6	886	1 NIA1_SOYBN	P54233 glycine max
57	31	88.6	890	1 NIA2_SOYBN	P39870 glycine max
58	31	88.6	1050	1 LKTA_ACTAC	P14662 actinobacil
59	31	88.6	1235	1 VGL2_CVMJH	P11225 murine coro
60	31	88.6	1324	1 VGL2_CVMA5	P11224 murine coro
61	31	88.6	1376	1 VGL2_CVM4	P22432 murine coro
62	31	88.6	1376	1 VGL2_CVMJC	Q02385 murine coro
63	31	88.6	1586	1 SN22_HUMAN	P51531 homo sapien
64	31	88.6	1647	1 SN24_HUMAN	P51532 homo sapien
65	30	85.7	478	1 KYNH_CABEL	Q18026 caenorhabdi
66	30	85.7	568	1 FLP_ZYGB1	P13784 zygoacchar
67	30	85.7	612	1 PEX5_YEAST	P35056 saccharomyc
68	30	85.7	722	1 GUNF_CLOCE	P37698 clostridium
69	30	85.7	843	1 ENV_HV1Y2	P35961 human immun
70	30	85.7	856	1 ENV_HV1Z8	P05881 human immun
71	30	85.7	867	1 ENV_HV1J3	P12489 human immun
72	30	85.7	891	1 NIA7_HORVU	P27968 hordeum vul
73	30	85.7	897	1 SYI_FERPE	Q9kdb4 ferrobact
74	30	85.7	904	1 NIA1_TOBAC	P11605 nicotiana t
75	30	85.7	904	1 NIA2_TOBAC	P08509 nicotiana t
76	30	85.7	909	1 NIA_PETHY	P36859 petunia hyb
77	30	85.7	939	1 SYI_BUCBP	Q89a59 buchnera ap
78	30	85.7	940	1 SYI_BUCAI	P57249 buchnera ap
79	30	85.7	2507	1 NBEA_CABEL	Q19317 caenorhabdi
80	30	85.7	4910	1 MDN1_YEAST	Q12019 saccharomyc
81	29	82.9	129	1 RS1A_DICDI	P46793 dictyosteli
82	29	82.9	160	1 NIA_LOTTE	P39882 lotus tetra
83	29	82.9	255	1 RECO_LISMO	Q8y752 listeria mo
84	29	82.9	283	1 RPCI_BPP1	P13121 bacterioph
85	29	82.9	283	1 RPCI_BPP7	P13122 bacterioph
86	29	82.9	326	1 Y338_CHLMU	Q9pkx2 chlamydia m
87	29	82.9	401	1 ASSY_XYLFA	Q9pem9 xyella fas
88	29	82.9	401	1 ASSY_XYLFT	P59606 xyella fas
89	29	82.9	445	1 MESJ_BUCAP	Q8ka23 buchnera ap
90	29	82.9	494	1 COAT_CERV	P05399 carnation e
91	29	82.9	531	1 NKFF3_HUMAN	Q9h4d5 homo sapien
92	29	82.9	565	1 CN1A_MOUSE	Q61481 mus musculu
93	29	82.9	623	1 SKLJ_HUMAN	Q81y47 homo sapien
94	29	82.9	630	1 SYR_PYRAE	Q8zta8 pyrobaculum
95	29	82.9	808	1 PDA1_TOBAC	P93400 nicotiana t
96	29	82.9	809	1 PDA1_VIGUN	Q04865 vigna ungu
97	29	82.9	812	1 PDA1_MAIZE	Q43270 zea mays (m
98	29	82.9	890	1 NIA1_PHAVU	P39866 phaseolus v
99	29	82.9	898	1 NIA_BETAV	P27783 betula verr
100	29	82.9	900	1 NIA_LOTJA	P39869 lotus japon
101	29	82.9	911	1 NIA_LYCES	P17570 lycopersico
102	29	82.9	918	1 NIA_CUCNA	P17569 cucurbita m
103	29	82.9	920	1 NIA_CICIN	P43101 cichorium i
104	29	82.9	1132	1 VHSJ_LAMBD	P03749 bacterioph
105	29	82.9	1337	1 YDM5_SCHPO	P87136 schizosacch
106	28	80.0	109	1 PHS_VIBCH	Q9klb9 vibrio chol

107	28	80.0	140	1	LYSS DROME	P37160 drosophila	180	27	77.1	292	1	Y240 MYCGE	P47482 mycoplasma
108	28	80.0	155	1	Y4A4_PSEAE	Q9hx23 pseudomonas	181	27	77.1	306	1	MNTA_BACSU	O34385 bacillus su
109	28	80.0	155	1	YCC6_PSEPK	Q88d17 pseudomonas	182	27	77.1	309	1	P2AA_CHICK	P48463 gallus gall
110	28	80.0	155	1	YCC6_PSEPK	Q88d17 pseudomonas	183	27	77.1	309	1	P2AA_HUMAN	P05323 homo sapien
111	28	80.0	173	1	NUDH_RHTLO	Q98f04 rhizobium 1	184	27	77.1	309	1	P2AA_MOUSE	P13353 mus musculu
112	28	80.0	191	1	NADD_STAEP	Q8cscl staphylococ	185	27	77.1	309	1	P2AB_HUMAN	P11082 homo sapien
113	28	80.0	194	1	HAM2_BACHD	Q9k8d9 bacillus ha	186	27	77.1	309	1	P2AB_RABIT	P11611 cryptotagus
114	28	80.0	195	1	OBL_OBELO	Q27709 obelia long	187	27	77.1	320	1	CCSA_MARPO	P12214 marchantia
115	28	80.0	200	1	ENGB_CLOAB	Q37fu0 clostridium	188	27	77.1	324	1	Y518_CHLPN	Q9z834 chlamydia p
116	28	80.0	200	1	NADD_CLOAB	Q57fj12 clostridium	189	27	77.1	335	1	TRD2_SPRCO	Q9z4w9 streptomyce
117	28	80.0	281	1	MODD_HAEIN	Q57278 haemophilus	190	27	77.1	348	1	YLM1_CABEL	P34404 caenorhabdi
118	28	80.0	281	1	MODD_HAEIN	Q57278 haemophilus	191	27	77.1	381	1	YJ04_SCHPO	O74405 schizosacch
119	28	80.0	283	1	PY97_CABEL	Q09245 caenorhabdi	192	27	77.1	382	1	DXR_CHLTE	O8kg43 chlorobium
120	28	80.0	327	1	CI30_MOUSE	Q9y375 homo sapien	193	27	77.1	390	1	ADHB_CLOAB	O44945 clostridium
121	28	80.0	328	1	CI30_MOUSE	Q9cwx2 mus musculu	194	27	77.1	400	1	DFP_HAEN	P44953 haemophilus
122	28	80.0	339	1	YNZ8_CABEL	P45968 caenorhabdi	195	27	77.1	404	1	DXR_PROMP	Q7v0w0 prochloroco
123	28	80.0	348	1	LLY_LEGPN	Q53407 legionella	196	27	77.1	406	1	CAIB_PROSL	O8gb19 proteus sp.
124	28	80.0	370	1	RECF_BACSU	P05651 bacillus su	197	27	77.1	409	1	Y148_MYCGE	P47394 mycoplasma
125	28	80.0	372	1	RE2_SYNY3	P74476 synecocyst	198	27	77.1	437	1	NEOR_STRCY	P14501 streptomyce
126	28	80.0	374	1	RECF_LACPL	Q890k5 lactobacill	199	27	77.1	445	1	Y148_MYCPN	P75584 mycoplasma
127	28	80.0	377	1	MTC3_CHVNI	P10835 chlorella v	200	27	77.1	487	1	C135_DROME	Q9vgb5 drosophila
128	28	80.0	406	1	DFP_ECOLI	Q10514 mycobacteri	201	27	77.1	499	1	GAG_HVIEL	P04592 human immun
129	28	80.0	445	1	DHE2_PORGI	P24285 escherichia	202	27	77.1	500	1	GAG_HVIRH	P05890 human immun
130	28	80.0	457	1	CFXA_ECOLI	Q03578 porphyromon	203	27	77.1	514	1	CP24_HUMAN	Q07973 homo sapien
131	28	80.0	499	1	GAG_HV1C4	P08336 escherichia	204	27	77.1	514	1	CP24_MOUSE	Q64441 mus musculu
132	28	80.0	499	1	GAG_HV1H2	P05887 human immun	205	27	77.1	514	1	CP24_RAT	Q09128 rattus norv
133	28	80.0	499	1	GAG_HV1J3	P12494 human immun	206	27	77.1	522	1	Z454_HUMAN	Q8n9f8 homo sapien
134	28	80.0	503	1	GAG_HV1J3	P20873 human immun	207	27	77.1	532	1	IP47_SHIFL	P18014 shigella fl
135	28	80.0	506	1	GAG_HV1WN	P05888 human immun	208	27	77.1	537	1	IP47_SHIFL	Q92197 rickettsia
136	28	80.0	511	1	GAG_HV1B1	P03347 human immun	209	27	77.1	556	1	BETA_ECOLI	P17444 escherichia
137	28	80.0	511	1	GAG_HV1B1	P04593 human immun	210	27	77.1	560	1	YF31_SCHPO	Q10484 schizosacch
138	28	80.0	511	1	GAG_HV1B1	P03348 human immun	211	27	77.1	565	1	MAOX_SCHPO	P43075 schizosacch
139	28	80.0	511	1	GAG_HV1PV	P03350 human immun	212	27	77.1	571	1	YK18_YEAST	P36076 saccharomyc
140	28	80.0	533	1	UBIB_PSEAE	Q9nub8 pseudomonas	213	27	77.1	574	1	IPA4_SHIFL	P18009 shigella fl
141	28	80.0	620	1	SMP_COTJA	Q2154 coturnix co	214	27	77.1	578	1	TREA_RABIT	P19813 oryctolagus
142	28	80.0	623	1	YD54_MYCTU	Q11024 mycobacteri	215	27	77.1	586	1	PYRG_RICPR	Q924f1 rickettsia
143	28	80.0	650	1	TDR3_MOUSE	Q1w18 mus musculu	216	27	77.1	587	1	GOX_PENAG	P81156 penicillium
144	28	80.0	725	1	MAZ2_PSESM	Q87z72 pseudomonas	217	27	77.1	596	1	GOX_TALFL	Q9w2m2 drosophila
145	28	80.0	808	1	PIA1_FIMBR	O4883 pimpinella	218	27	77.1	605	1	ASH2_MOUSE	Q92452 talaromyc
146	28	80.0	917	1	PIA2_ARATH	P1035 arabidopsis	219	27	77.1	623	1	ASH2_MOUSE	Q91x20 mus musculu
147	28	80.0	956	1	SVY_TREPA	O83998 treponema p	220	27	77.1	628	1	ASH2_HUMAN	Q9ub13 homo sapien
148	28	80.0	1004	1	MYV10_MOUSE	P23249 mus musculu	221	27	77.1	639	1	YKPS_YEAST	P36056 saccharomyc
149	28	80.0	1227	1	LAF4_HUMAN	P51826 homo sapien	222	27	77.1	639	1	YKPS_YEAST	Q46840 escherichia
150	28	80.0	1272	1	FMR2_MOUSE	O5112 mus musculu	223	27	77.1	651	1	KEL3_YEAST	Q08979 saccharomyc
151	28	80.0	1297	1	SOS2_MOUSE	Q02384 mus musculu	224	27	77.1	661	1	ARK5_HUMAN	P60285 homo sapien
152	28	80.0	1311	1	FMR2_HUMAN	P51816 homo sapien	225	27	77.1	684	1	ISH1_SCHPO	Q9y7x6 schizosacch
153	28	80.0	1319	1	SOS1_MOUSE	Q62245 mus musculu	226	27	77.1	756	1	K6PF_CABEL	Q27483 caenorhabdi
154	28	80.0	1332	1	RPO_SMYEA	P28897 strawberry	227	27	77.1	770	1	COG7_HUMAN	P83436 homo sapien
155	28	80.0	1332	1	SOS2_HUMAN	Q07890 homo sapien	228	27	77.1	843	1	PIW1_DROME	Q9vkm1 drosophila
156	28	80.0	1333	1	SOS1_HUMAN	Q07889 homo sapien	229	27	77.1	851	1	MUTS_YERPE	Q8zbq3 yersinia pe
157	28	80.0	1430	1	PPU0_HUMAN	Q92729 homo sapien	230	27	77.1	853	1	MUTS_ECO57	Q86p98 escherichia
158	28	80.0	2145	1	US20_CABEL	Q9u290 caenorhabdi	231	27	77.1	853	1	MUTS_ECOLI	Q8fel3 escherichia
159	28	80.0	2363	1	SPCO_MOUSE	Q62261 mus musculu	232	27	77.1	853	1	MUTS_ECOLI	Q23909 escherichia
160	28	80.0	2364	1	SPCO_HUMAN	Q01082 homo sapien	233	27	77.1	853	1	MUTS_VIBPA	Q871q9 vibrio para
161	28	80.0	3712	1	ACVS_CEPAC	P25464 cephalospor	234	27	77.1	855	1	MUTS_SALTY	P10339 salmonella
162	28	80.0	64	1	VRAL_BPP22	P14113 bacterioph	235	27	77.1	860	1	MUTS_PASMU	P57972 pasteurella
163	27	77.1	66	1	VRAL_LAMB2	P03703 bacterioph	236	27	77.1	861	1	MUTS_HARIN	P44834 haemophilus
164	27	77.1	76	1	VRAL_BPPH3	P07235 bacterioph	237	27	77.1	862	1	MUTS_VIRCH	Q9ku16 vibrio chol
165	27	77.1	100	1	Y939_AERPE	Q9ydh4 aeropyrum p	238	27	77.1	876	1	SYL_AGR75	Q8ubv2 agrobacteri
166	27	77.1	103	1	RS10_CHLTE	Q8kah1 chlorobium	239	27	77.1	916	1	SCRB_LIMPO	Q25386 limulus pol
167	27	77.1	151	1	RS10_DROME	Q9nlp6 drosophila	240	27	77.1	917	1	CP3_DROME	Q9xyp8 drosophila
168	27	77.1	152	1	YAI1_ECOLI	P52088 escherichia	241	27	77.1	925	1	PDC2_YEAST	P32896 saccharomyc
169	27	77.1	163	1	E1B5_ADE12	P04492 human adeno	242	27	77.1	937	1	SVI_ECOLI	P00956 escherichia
170	27	77.1	208	1	RS6_MYCGE	P47336 mycoplasma	243	27	77.1	938	1	SVI_EUCAP	Q8k922 buchnera ap
171	27	77.1	214	1	NADD_BUCAL	P57521 buchnera ap	244	27	77.1	941	1	SVI_HAEIN	P43824 haemophilus
172	27	77.1	243	1	CLCA_BOVIN	P04973 bos taurus	245	27	77.1	943	1	SVI_HAEIN	P43824 haemophilus
173	27	77.1	255	1	PPA1_LYCES	P27061 lycopersico	246	27	77.1	958	1	SIT_PSEFL	P18330 pseudomonas
174	27	77.1	263	1	INMT_HUMAN	Q95050 homo sapien	247	27	77.1	1003	1	HW10_HUMAN	Q09101 drosophila
175	27	77.1	264	1	NNWT_HUMAN	P40261 homo sapien	248	27	77.1	1066	1	AOSL_PLSHO	Q9hcel homo sapien
176	27	77.1	265	1	OTSB_RHISN	P55611 rhizobium s	249	27	77.1	1092	1	DPD_DROME	O16025 plexaura ho
177	27	77.1	270	1	TCMP_STRGA	P39887 streptomyce	250	27	77.1	1148	1	POLN_RVVT	P54358 drosophila
178	27	77.1	290	1	Y634_XYLFT	Q8vdp8 xyella fas	251	27	77.1	1150	1	NRDC_HUMAN	P13888 ross river
179	27	77.1	290	1	YE05_XYLFA	Q9pdh4 xyella fas	252	27	77.1				O43847 homo sapien

253	27	77.1	1157	1	JTP_CABEL	P34609	caenorhabdi	326	26	74.3	261	1	NIF3_HUMAN	Q9gzv7	homo sapien
254	27	77.1	1161	1	NRDC_MOUSE	Q8bhg1	mus musculus	327	26	74.3	261	1	NIF3_MOUSE	P58466	mus musculus
255	27	77.1	1161	1	NRDC_RAT	P47245	rattus norv	328	26	74.3	269	1	PF11_HUMAN	Q00169	homo sapien
256	27	77.1	1353	1	VGL2_CVHOC	P36334	human coron	329	26	74.3	269	1	PP11_RABIT	P48738	oryctolagus
257	27	77.1	1359	1	STH1_YEAST	P32597	saccharomyc	330	26	74.3	270	1	PP11_MOUSE	P53810	mus musculus
258	27	77.1	1363	1	VGL2_CVBP	P25190	bovine coro	331	26	74.3	270	1	PP11_RAT	P16446	rattus norv
259	27	77.1	1363	1	VGL2_CVBL9	P25191	bovine coro	332	26	74.3	290	1	Y084_MYCSE	P47330	mycoplasma
260	27	77.1	1363	1	VGL2_CVBL9	P25192	bovine coro	333	26	74.3	291	1	SC17_YEAST	P32602	saccharomyc
261	27	77.1	1363	1	VGL2_CVBM	P15777	bovine coro	334	26	74.3	294	1	239F_HUMAN	Q15777	homo sapien
262	27	77.1	1363	1	VGL2_CVBQ	P25193	bovine coro	335	26	74.3	294	1	DAPA_RICTY	Q9ake4	rickettsia
263	27	77.1	1363	1	VGL2_CVBV	P25194	bovine coro	336	26	74.3	294	1	UNG_HSV23	P13158	herpes simp
264	27	77.1	1443	1	DP03_MYCPN	P75080	mycoplasma	337	26	74.3	295	1	TSR2_MOUSE	Q8k3v1	mus musculus
265	27	77.1	1499	1	PGP1_HUMAN	Q9y498	homo sapien	338	26	74.3	296	1	CI30_DROME	Q9vail	drosophila
266	27	77.1	1539	1	BPT1_YEAST	P14772	saccharomyc	339	26	74.3	301	1	RPC6_SCHPO	Q94553	schizosacch
267	27	77.1	1638	1	BRM_DROME	P25439	drosophila	340	26	74.3	303	1	SPRC_HUMAN	P09486	homo sapien
268	27	77.1	1947	1	MYSC_CABEL	P12845	caenorhabdi	341	26	74.3	304	1	SPRC_BOVIN	P31213	bos taurus
269	27	77.1	2472	1	SPCN_HUMAN	Q13813	homo sapien	342	26	74.3	305	1	LPXC_ECOLI	P07652	escherichia
270	27	77.1	2472	1	SPCN_RAT	P16085	rattus norv	343	26	74.3	305	1	LPXC_HAERIN	P45070	haemophilus
271	27	77.1	2479	1	POLN_RRVN	P13887	ross river	344	26	74.3	305	1	LPXC_PASMU	Q8z9p5	pasteurella
272	27	77.1	3343	1	BRC2_RAT	Q35923	rattus norv	345	26	74.3	305	1	LPXC_SALTI	Q8z9p5	salmonella
273	26	74.3	55	1	SRY_MACFA	P36391	macaca fasc	346	26	74.3	306	1	LPXC_SALTY	Q8z9p5	salmonella
274	26	74.3	81	1	MOAD_HAERIN	P45309	haemophilus	347	26	74.3	306	1	LPXC_VIBCH	Q8z9p5	shewanella
275	26	74.3	92	1	V05_VACC8	P24284	vaccinia vi	348	26	74.3	305	1	LPXC_VIBPA	Q8z9p5	vibrio para
276	26	74.3	108	1	Y04B_BP74	P07082	bacterioph	349	26	74.3	305	1	LPXC_VIBVU	Q8z9p5	vibrio vuln
277	26	74.3	113	1	YBBY_ECOLI	P76277	escherichia	350	26	74.3	305	1	TSR2_HUMAN	Q8z9p5	homo sapien
278	26	74.3	115	1	Y440_ARCFU	Q29809	archaeoglob	351	26	74.3	306	1	DDL_BUCAP	Q51927	buchnera ap
279	26	74.3	119	1	THH2_BRANA	Q39362	brassica na	352	26	74.3	306	1	LPXC_SHERON	Q8z9p5	shewanella
280	26	74.3	121	1	VNS2_INCAA	Q01640	influenza c	353	26	74.3	306	1	LPXC_YERPE	Q8z9p5	yersinia pe
281	26	74.3	121	1	VNS2_INCUJ	P12603	influenza c	354	26	74.3	308	1	ERA_BRAJA	Q59162	bradyrhizob
282	26	74.3	122	1	YHDN_ECOLI	P36677	escherichia	355	26	74.3	309	1	CIWG_HUMAN	Q8z9p5	homo sapien
283	26	74.3	131	1	HSLR_HAERIN	P44754	haemophilus	356	26	74.3	309	1	KHSE_BACSU	Q8z9p5	bacillus su
284	26	74.3	132	1	HSLR_AERSA	Q44264	aeromonas s	357	26	74.3	310	1	OSAR_HUMAN	Q8z9p5	homo sapien
285	26	74.3	133	1	HSLR_ECOLI	P45802	escherichia	358	26	74.3	310	1	OC09_YEAST	Q8z9p5	mus musculus
286	26	74.3	133	1	REV_CAEV	P31628	caprine art	359	26	74.3	316	1	YCF9_YEAST	P25586	saccharomyc
287	26	74.3	133	1	REV_CAEV	P33460	caprine art	360	26	74.3	317	1	V05_VACC0	P24084	vaccinia vi
288	26	74.3	142	1	LYSX_DROME	P37161	drosophila	361	26	74.3	317	1	V05_VACC0	P24084	vaccinia vi
289	26	74.3	162	1	XYLB_AMFSP	P54271	ampullariel	362	26	74.3	317	1	V05_VACC0	P24084	vaccinia vi
290	26	74.3	166	1	ING_MARMO	Q35735	marmota mon	363	26	74.3	317	1	V05_VACC0	P24084	vaccinia vi
291	26	74.3	167	1	CD3D_SHEEP	P18438	ovis aries	364	26	74.3	319	1	CCSA_OENHO	Q01227	vaccinia vi
292	26	74.3	172	1	Y819_PASMU	Q9cmk4	pasteurella	365	26	74.3	319	1	COBD_BACHD	Q9cmk4	oenothea ha
293	26	74.3	176	1	DSBB_ECOLI6	P59343	escherichia	366	26	74.3	319	1	FABG_ARATH	Q9kci3	bacillus ha
294	26	74.3	176	1	DSBB_ECOLI	P30018	escherichia	367	26	74.3	327	1	YG29_SYNY3	P32027	arabidopsis
295	26	74.3	176	1	DSBB_SHIFL	Q4155	shigella fl	368	26	74.3	329	1	YCLC_PSEPU	P74346	synecocyst
296	26	74.3	176	1	DSBB_YERPE	Q8z9p5	yersinia pe	369	26	74.3	334	1	UNG_HSV11	Q47100	pseudomonas
297	26	74.3	176	1	VA22_VACC0	P20997	vaccinia vi	370	26	74.3	339	1	R13A_ARATH	P3157	a glucan en
298	26	74.3	178	1	ELBS_ADE07	P03248	human adeno	371	26	74.3	339	1	STEA_HUMAN	Q9zue8	homo sapien
299	26	74.3	181	1	CU25_HUMAN	Q9y426	homo sapien	372	26	74.3	339	1	YTH6_RHOER	P43484	rhodococcus
300	26	74.3	182	1	YCY0_YEAST	P25654	saccharomyc	373	26	74.3	340	1	Y574_CABEL	Q93618	caenorhabdi
301	26	74.3	183	1	Y171_BURCE	P24577	burkholderi	374	26	74.3	343	1	YN93_ANASP	P46079	anaeana ap
302	26	74.3	187	1	VA22_VARV	P33845	variola vir	375	26	74.3	344	1	GPDA_OCEIH	Q8z9p5	oceanobacil
303	26	74.3	205	1	YB23_METJA	Q58523	methanococ	376	26	74.3	346	1	PRIS_PYRHO	Q57934	pyrococcus
304	26	74.3	206	1	GIDB_YERPE	Q8z9p5	yersinia pe	377	26	74.3	347	1	PRIS_PYRPU	Q57934	pyrococcus
305	26	74.3	210	1	GIDB_VIBCH	Q8z9p5	vibrio chol	378	26	74.3	350	1	YCY3_METJA	Q58669	methanococ
306	26	74.3	211	1	GIDB_VIBPA	Q8z9p5	vibrio para	379	26	74.3	353	1	RRPO_FVSP	P22657	potato viru
307	26	74.3	211	1	YF78_CABEL	Q92224	caenorhabdi	380	26	74.3	364	1	F16P_XANFL	P3014	xanthobacte
308	26	74.3	212	1	DSBI_SHEON	Q8z9p5	shewanella	381	26	74.3	365	1	SOXB_RHOSO	P54997	rhodococcus
309	26	74.3	212	1	RL10_PIG	Q29195	sus scrofa	382	26	74.3	374	1	MTB1_BACBR	P34905	bacillus br
310	26	74.3	213	1	RL10_BOVIN	Q8z9p5	bos taurus	383	26	74.3	376	1	KAPR_DROME	P16905	drosophila
311	26	74.3	213	1	RL10_HUMAN	P27635	homo sapien	384	26	74.3	377	1	KAPR_APLCA	P31319	aplysia cal
312	26	74.3	213	1	RL10_MOUSE	P45634	mus musculus	385	26	74.3	378	1	AGAL_COFAR	Q42656	coffea arab
313	26	74.3	223	1	RACE_DICTDI	Q23862	dictyosteli	386	26	74.3	379	1	KAP0_BOVIN	P00514	bos taurus
314	26	74.3	224	1	CTH8_HUMAN	Q9d444	homo sapien	387	26	74.3	379	1	KAP0_PIG	P07802	sus scrofa
315	26	74.3	224	1	CTH8_MOUSE	Q9d8b3	mus musculus	388	26	74.3	380	1	KAP0_RAT	P09456	rattus norv
316	26	74.3	226	1	SP25_CANFA	Q28250	canis fami	389	26	74.3	381	1	KAP0_HUMAN	P10644	homo sapien
317	26	74.3	226	1	SP25_HUMAN	Q15005	homo sapien	390	26	74.3	384	1	CGB3_CABEL	Q10654	caenorhabdi
318	26	74.3	226	1	SP25_MOUSE	Q29yn2	mus musculus	391	26	74.3	385	1	DXR1_BACAA	Q8n10	bacillus an
319	26	74.3	228	1	RNFG_PSEST	Q9evn3	pseudomonas	392	26	74.3	385	1	DXR1_BACBR	Q8n10	bacillus an
320	26	74.3	229	1	UNG_COXBU	Q83cw4	coxiella bu	393	26	74.3	385	1	YK30_MYCLE	Q69481	mycobacteri
321	26	74.3	230	1	ALKL_PSEOL	Q00595	pseudomonas	394	26	74.3	388	1	PURK_SYNY3	P74724	synecocyst
322	26	74.3	250	1	PECB_SCHGR	P82886	schistosom	395	26	74.3	389	1	GALT_BUTPI	P45981	butyrivibri
323	26	74.3	252	1	AGGD_ECOLI	P46004	escherichia	396	26	74.3	394	1	TYRB_PARDE	P95468	paracoccus
324	26	74.3	255	1	RECO_LISTIN	Q22bq0	listeria in	397	26	74.3	397	1	ASSY_XANCP	Q8p8j4	xanthomonas
325	26	74.3	255	1	UNG_HSV2H	P28275	herpes simp	398	26	74.3	408	1	EFTU_GUITH	P19457	guillardia

399 26 74.3 411 1 AGAL_CYATE
 400 26 74.3 411 1 VG66_HSV11
 401 26 74.3 412 1 ASSY_XANAC
 402 26 74.3 413 1 AMP2_BACST
 403 26 74.3 413 1 SIAL_CHICK
 404 26 74.3 414 1 MTNW_BACSU
 405 26 74.3 420 1 RBL_FYRFU
 406 26 74.3 424 1 RBL_PYRAB
 407 26 74.3 429 1 PEPB_VIBCH
 408 26 74.3 432 1 PEPB_VIBPA
 409 26 74.3 432 1 R114_SACPA
 410 26 74.3 434 1 V023_F0WVP
 411 26 74.3 435 1 DHE4_HALSA
 412 26 74.3 435 1 R114_YEAST
 413 26 74.3 437 1 ENCB_VIBVU
 414 26 74.3 439 1 SYE2_HELPVJ
 415 26 74.3 443 1 KSN2_HUMAN
 416 26 74.3 443 1 KYN2_YEAST
 417 26 74.3 451 1 K6PF_THELI
 418 26 74.3 459 1 HNF6_HUMAN
 419 26 74.3 465 1 HNF6_MOUSE
 420 26 74.3 465 1 HNF6_RAT
 421 26 74.3 471 1 GATH_SCHPO
 422 26 74.3 471 1 RCA_SPIOL
 423 26 74.3 475 1 YMT4_YEAST
 424 26 74.3 480 1 AGLA_THEMA
 425 26 74.3 482 1 PCD7_MOUSE
 426 26 74.3 485 1 PCD7_HUMAN
 427 26 74.3 487 1 YFGC_ECOS7
 428 26 74.3 487 1 YFGC_ECOS7
 429 26 74.3 487 1 YFGC_ECOLI
 430 26 74.3 490 1 C883_ARATH
 431 26 74.3 493 1 GLO3_YEAST
 432 26 74.3 496 1 SYE_PSEAE
 433 26 74.3 496 1 PCP_HUMAN
 434 26 74.3 499 1 ABFB_ASPNG
 435 26 74.3 500 1 DPP2_RAT
 436 26 74.3 502 1 LAS1_YEAST
 437 26 74.3 504 1 CP42_YEAT
 438 26 74.3 504 1 YM68_YEAST
 439 26 74.3 506 1 DPP2_MOUSE
 440 26 74.3 507 1 CP43_RAT
 441 26 74.3 507 1 EPOR_MOUSE
 442 26 74.3 508 1 CP48_RAT
 443 26 74.3 508 1 EPOR_HUMAN
 444 26 74.3 509 1 CP41_RAT
 445 26 74.3 509 1 Y795_HUMAN
 446 26 74.3 510 1 CP46_RABIT
 447 26 74.3 511 1 CP45_RABIT
 448 26 74.3 511 1 CP4B_HUMAN
 449 26 74.3 511 1 CP4B_MOUSE
 450 26 74.3 511 1 CP4B_RAT
 451 26 74.3 511 1 U171_CABEL
 452 26 74.3 512 1 ALDB_ECOLI
 453 26 74.3 512 1 CP4Y_HUMAN
 454 26 74.3 519 1 CPFC_HUMAN
 455 26 74.3 529 1 CN1A_BOVIN
 456 26 74.3 532 1 GSI_NEUCR
 457 26 74.3 534 1 CN1A_HUMAN
 458 26 74.3 538 1 TCMA_STRGA
 459 26 74.3 545 1 AMDS_ASPOR
 460 26 74.3 545 1 CP10_LYMTS
 461 26 74.3 547 1 YQJ1_ECOLI
 462 26 74.3 551 1 CBX4_MOUSE
 463 26 74.3 551 1 OPGD_SALTI
 464 26 74.3 551 1 OPGD_SALTY
 465 26 74.3 552 1 YGXB_BACSU
 466 26 74.3 558 1 CBX4_HUMAN
 467 26 74.3 558 1 VB04_VARV
 468 26 74.3 566 1 SYRD_PSESY
 469 26 74.3 573 1 DPOL_MOUSE
 470 26 74.3 575 1 DPOL_HUMAN
 471 26 74.3 575 1 VG05_BPT4

472 26 74.3 582 1 VATA_DEIRA
 473 26 74.3 587 1 GGT_BACSU
 474 26 74.3 589 1 C49A_DROME
 475 26 74.3 590 1 SYD_SALTI
 476 26 74.3 590 1 SYD_SALTY
 477 26 74.3 591 1 SYR_BORBU
 478 26 74.3 592 1 SVC2_RAT
 479 26 74.3 593 1 GRN_HUMAN
 480 26 74.3 600 1 GLMS_STAAM
 481 26 74.3 600 1 GLMS_STAAM
 482 26 74.3 607 1 VATA_NEUCR
 483 26 74.3 619 1 MUTL_XYLFA
 484 26 74.3 619 1 MUTL_XYLFT
 485 26 74.3 620 1 ACE1_CAEER
 486 26 74.3 620 1 ACE1_CABEL
 487 26 74.3 620 1 KHL8_HUMAN
 488 26 74.3 623 1 PTR2_CANAL
 489 26 74.3 624 1 MUTL_XANCP
 490 26 74.3 624 1 PTMA_PASMU
 491 26 74.3 629 1 KHL8_MOUSE
 492 26 74.3 633 1 GYP3_YEAST
 493 26 74.3 647 1 SVC2_MOUSE
 494 26 74.3 650 1 SVC2_HUMAN
 495 26 74.3 660 1 DNL2_CHIMU
 496 26 74.3 686 1 KITH_HSVBM
 497 26 74.3 691 1 YHJG_ECOLI
 498 26 74.3 692 1 RFX2_MOUSE
 499 26 74.3 701 1 YL66_YEAST
 500 26 74.3 709 1 CN1C_HUMAN

Q9rhwg deinococcus
 P54422 bacillus su
 Q9v513 drosophila
 Q825w1 salmonella
 Q8zrv2 salmonella
 O51540 borrelia bu
 Q9wtw8 rattus norv
 P28799 h granulins
 Q99as5 s glucosami
 Q8nve6 s glucosami
 P11592 neurospora
 Q9f5b8 xylolla fas
 Q87ac9 xylolla fas
 Q27459 caenorhabdi
 P38433 caenorhabdi
 Q9p2g9 homo sapien
 P46030 candida alb
 Q8p8e4 xanthomonas
 Q9c1y8 pasteurella
 P59280 mus musculu
 P48566 saccharomyc
 Q9epir4 mus musculu
 Q9ugh3 homo sapien
 Q9p8p2 chlamydia m
 P33802 bovine herp
 P37645 escherichia
 P48379 mus musculu
 Q06149 saccharomyc
 Q14123 homo sapien

ALIGNMENTS

RESULT 1
 KYN RAT
 ID KYN RAT STANDARD; PRT; 464 AA.
 AC P70712; Q9QW90;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
 GN KYN.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
 [1]

RN SEQUENCE, AND MASS SPECTROMETRY.

RP STRAIN=Wistar; TISSUE=Liver;
 RC MEDLINE=96049498; PubMed=7578221;

RA Takeuchi F., Tsubouchi R., Yoshino M., Shibata Y.;
 "Amino-acid sequence of rat liver kynureninase.";

RL Biochim. Biophys. Acta 1252:185-188(1995).
 [2]

RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RP TISSUE=Liver;
 RC MEDLINE=97324088; PubMed=9180257;

RA Tona S., Nakamura M., Tone S., Okuno E., Kido R., Breton J.,
 Avanzi N., Cozzi L., Speciale C., Mostardini M., Gatti S., Benatti L.;

RT "Cloning and recombinant expression of rat and human kynureninase.";

RL FEBS Lett. 408:5-10(1997).
 [3]

RN SEQUENCE OF 19-117 FROM N.A., AND PARTIAL SEQUENCE.

RP TISSUE=Kidney, and Liver;
 RC MEDLINE=963114506; PubMed=8706755;

RA Alberati-Giani D., Buchli R., Malherbe P., Broger C., Lang G.,
 Koehler C., Lahm H.-W., Cesura A.M.;

RT "Isolation and expression of a cDNA clone encoding human
 kynureninase.";

RL Eur. J. Biochem. 239:460-468(1996).
 CC -!- FUNCTION: Catalyzes the cleavage of L-kynurenine (L-KYN) and L-3-
 hydroxykynurenine (L-3OHKYN) into anthranilic (AA) and 3-

CC hydroxyanthranilic acids (3-OHAA), respectively. Has a preference
 CC for the L-3-hydroxy form. Optimum activity is around pH 9.0 for L-
 CC kyn and around 8.5 for L-3OHKYN. Also has cysteine-conjugate-
 CC beta-lyase activity.
 CC -1- CATALYTIC ACTIVITY: L-kynurenine + H(2)O = anthranilate + L-
 CC alanine.
 CC -1- CATALYTIC ACTIVITY: L-3-hydroxykynurenine + H(2)O = 3-
 CC hydroxyanthranilate + L-alanine.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- ENZYME REGULATION: Inhibited by o-methylbenzoylalanine (OMBA).
 CC -1- PATHWAY: Involved in the biosynthesis of NAD cofactors from
 CC tryptophan through the kynurenine pathway.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: High levels in liver and kidney. Also
 CC detected in heart, retina, ovary, lung, testis and brain.
 CC -1- INDUCTION: Inhibited by thiol reagents and heavy metal ions.
 CC -1- SIMILARITY: BELONGS TO THE KYURENINASE FAMILY, SLIGHTLY RELATED
 CC TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
 CC -----
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 CC -----
 CC EMBL; U68168; AAC53206.1; -;
 CC PIR; S59898; S59898.
 CC PIR; T48675; T48675.
 CC KW Hydrolyase; Pyridoxal phosphate; Acetylation.
 CC FT MOD RES 1 276 PYRIDOXAL PHOSPHATE.
 CC FT BINDING 18 18 A -> T (IN REF. 1).
 CC FT CONFLICT 26 26 D -> N (IN REF. 1).
 CC FT CONFLICT 118 118 T -> S (IN REF. 1).
 CC FT CONFLICT 118 118 T -> S (IN REF. 1).
 CC SQ SEQUENCE 464 AA; 52453 MW; F1FC95E3202CEC CRC64;
 CC -----
 CC Query Match 100.0%; Score 35; DB 1; Length 464;
 CC Best Local Similarity 100.0%; Pred. No. 11;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Qy 1 ELDKWA 6
 CC Db 90 ELDKWA 95
 CC |||||
 CC
 CC RESULT 2
 CC ID_KYNU HUMAN STANDARD; PRT; 465 AA.
 CC AC Q16719;
 CC DT 15-DEC-1998 (Rel. 37, Created)
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC DE Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
 CC GN KYNU.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 CC RC TISSUE=Hepatoma;
 CC RX MEDLINE=96314506; PubMed=8706755;
 CC RA Alberati-Giani D., Buchli R., Malherbe P., Broger C., Lang G.,
 CC RA Kohler C., Lahm H.-W., Cesura A.M.;
 CC RT "Isolation and expression of a cDNA clone encoding human
 CC RT kynureninase.";
 CC RL Eur. J. Biochem. 239:460-468 (1996).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Liver;

RX MEDLINE=97324088; PubMed=9180257;
 RA Toma S., Nakamura M., Tone S., Okuno E., Kido R., Breton J.,
 RA Avanzi N., Cozzi L., Speciale C., Mostardini M., Gatti S., Benatti L.;
 RT "Cloning and recombinant expression of rat and human kynureninase.";
 RL FEBS Lett. 408:5-10 (1997).
 CC -1- FUNCTION: Catalyzes the cleavage of L-kynurenine (L-KYN) and L-3-
 CC hydroxykynurenine (L-3OHKYN) into anthranilic (AA) and 3-
 CC hydroxyanthranilic acids (3-OHAA), respectively. Has a preference
 CC for the L-3-hydroxy form. Also has cysteine-conjugate-beta-lyase
 CC activity (By similarity).
 CC -1- CATALYTIC ACTIVITY: L-kynurenine + H(2)O = anthranilate + L-
 CC alanine.
 CC -1- CATALYTIC ACTIVITY: L-3-hydroxykynurenine + H(2)O = 3-
 CC hydroxyanthranilate + L-alanine.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- ENZYME REGULATION: Inhibited by o-methoxybenzoylalanine (OMBA).
 CC -1- PATHWAY: Involved in the biosynthesis of NAD cofactors from
 CC tryptophan through the kynurenine pathway.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested (heart, brain
 CC placenta, lung, liver, skeletal muscle, kidney and pancreas).
 CC Highest levels found in placenta, liver and lung. Expressed in
 CC all brain regions.
 CC -1- INDUCTION: Increased levels in several cerebral and systemic
 CC inflammatory conditions.
 CC -1- SIMILARITY: BELONGS TO THE KYURENINASE FAMILY, SLIGHTLY RELATED
 CC TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U57721; AAC50650.1; -;
 CC PIR; G02652; G02652.
 CC Genew; HGNC:6469; KYNU.
 CC GK; Q16719; -;
 CC MW; 605197; -;
 CC MM; 236800; -;
 CC GO; GO:0008233; F:peptidase activity; TAS.
 CC GO; GO:0008233; F:peptidase activity; TAS.
 CC KW Hydrolyase; Pyridoxal phosphate; Acetylation.
 CC FT MOD RES 1 276 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC FT BINDING 276 276 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC SQ SEQUENCE 465 AA; 52351 MW; BDD136BE18C79EBB CRC64;
 CC -----
 CC Query Match 100.0%; Score 35; DB 1; Length 465;
 CC Best Local Similarity 100.0%; Pred. No. 11;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC Qy 1 ELDKWA 6
 CC Db 90 ELDKWA 95
 CC |||||
 CC
 CC RESULT 3
 CC ID_YR86 CAEEL STANDARD; PRT; 817 AA.
 CC AC Q09568;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Hypothetical protein F48E8.6 in chromosome III.
 CC GN F48E8.6.
 CC OS Caenorhabditis elegans.
 CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC OC Rhabditidae; Peloderinae; Caenorhabditis.
 CC OX NCBI_TaxID=6239;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.

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RC STRAIN-Bristol N2;
RA Kirsten J.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ribonuclease II (RNB) family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U23514; AAC4543.1; -.
DR PIR; T16409; T16409.
DR WormPep; F48E8.6; CE02758.
DR InterPro; IPR001900; Ribonuclease_II.
DR Pfam; PF00773; RNB; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
KW Hypothetical protein; Hydrolase; Nuclease.
SQ SEQUENCE 817 AA; 93727 MW; 9BESB06162699243 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 817;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 359 ELDKWA 364
|||||

RESULT 4
ENV_HV1ND STANDARD; PRT; 846 AA.
ID -ENV_HV1ND
AC P18799;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11695;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90034200; PubMed=2806917;
RA Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F.,
RA Hampe A., Chermann J.C.;
RT "Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the
RT human immunodeficiency virus."
RL Gene 81:275-284(1989).
CC -1- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH
CC AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M27323; AAA44873.1; -.
DR PIR; JQ0066; VCLJND.
DR HIV; M27323; ENV5NDK.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
FW SIGNAL.

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FT CHAIN 30 501
FT CHAIN 502 846
FT DISULFID 53 73
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FT CARBOHYD 627 627
SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2B83 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 846;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 652 ELDKWA 657
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RESULT 5
ENV_HV1S1 STANDARD; PRT; 847 AA.
ID -ENV_HV1S1
AC P19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation."
RL J. Virol. 64:4390-4398(1990).
CC -----
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QY 1 ELDKWA 6
 DB 653 ELDKWA 558
 RESULT 7
 ENV_HV1JR ENV_HV1JR STANDARD; PRT; 848 AA.
 AC P20871;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 DE GN ENV.
 OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11688;
 OX [1]
 RN SEQUENCE FROM N.A.
 RA Koyanagi S., Chen I.S.Y.;
 RA Submitted (DEC-1988) to the HIV data bank.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M38429; AAB03749.1; --
 DR PDB; 1CB4; 18-MAR-99.
 DR HIV; M38429; ENVJRCSF.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure. 1 32
 KW SIGNAL
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 FT CARBOHYD 1286 128

FT DISULFID 378 440 BY SIMILARITY.
 FT DISULFID 385 413 BY SIMILARITY.
 FT CARBOHYD 88 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 136 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 141 N-LINKED (GLCNAC. .) (POTENTIAL).
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 FT CARBOHYD 745 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 811 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

 Query Match 100.0%; Score 35; DB 1; Length 851;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ELDKWA 6
 Db 657 ELDKWA 662

 RESULT 9
 ENV_HV18N
 ID ENV_HV18N STANDARD; PRT; 852 AA.
 AC P12488;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11693;
 RN [1]
 RX SEQUENCE FROM N.A.
 RA MEDLINE=89085613; PubMed=2789516;
 RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P., Dandekar S.;
 RA "Biological and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive dementia.";
 RL Virology 168:79-89 (1989).
 CC -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
 CC -----
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 CC EMBL; M21098; AAA44221.1; -.
 DR PIR; A31667; VCLJBR.
 DR PDB; 1IM7; 23-OCT-02.
 DR HIV; M21098; ENV\$BRVA.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 KW 3D-structure.
 FT SIGNAL 1 30
 FT CHAIN 31 507 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 155 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.
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 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 670 670 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

 Query Match 100.0%; Score 35; DB 1; Length 852;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 ELDKWA 6
 Db 658 ELDKWA 663

 RESULT 10
 ENV_HV183
 ID ENV_HV183 STANDARD; PRT; 852 AA.
 AC P19549;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome.";
RL J. Virol. 64:4016-4020(1990).
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CC or send an email to license@isb-sib.ch).
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DR EMBL; AY352275; AAQ17031.1; -;
DR PDB; 1MEQ; 11-DEC-02.
DR HIV; M38427; ENV\$SF33.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 237 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CRC64;

Query Match 100.0%; Score 35; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 658 ELDKWA 663
RESULT 11
ENV_HV1EL STANDARD; PRT; 853 AA.
ID P04581;
AC 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RL Cell 46:63-74(1986).
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DR EMBL; K03454; AAA44329.1; -;
DR EMBL; A07108; CAA00616.1; -;
DR HIV; K03454; ENV\$ELI.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAA0D07A5 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 853;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 659 ELDKWA 664

RESULT 12
 ENV_HVMP STANDARD; PRT; 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamonic C., Mann A.M., Meier C.,
 Wasiak A.
 RA "Cloning and characterization of human immunodeficiency virus type 1
 variants diminished in the ability to induce syncytium-independent
 cytolysis.";
 RL J. Virol. 64:3792-3803 (1990).
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 CC -----
 CC EMBL; M33943; AAA44850.1; -.
 DR PDB; 1A1K; 16-JUN-97.
 DR HIV; M33943; ENV\$MFA.
 DR InterPro; IPR000328; ENV GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
 3D-structure.
 FT SIGNAL 1 309 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 31 509 TRANSMEMBRANE GLYCOPROTEIN.
 FT CHAIN 510 853 BY SIMILARITY.
 FT DISULFID 54 74
 FT DISULFID 119 203

FT DISULFID 126 194 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 329 BY SIMILARITY.
 FT DISULFID 376 443 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96912 MW; 337B993B6F22ABA CRC64;

Query Match 100.0%; Score 35; DB 1; Length 853;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
 |||||
 Db 660 ELDKWA 665

RESULT 13
 ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Theodore T., Buckler-White A.;
 RL Submitted (NOV-1988) to the HIV data bank.
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EMBL; M22639; AAA54370.1; -.
 PIR; S54384; S54384.
 DR PIR; M22639; ENV5226.
 DR InterPro; IPR000328; Env GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Transmembrane;
 KW Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 508
 FT CHAIN 509 853
 FT DISULFID 53 73
 FT DISULFID 118 206
 FT DISULFID 125 197
 FT DISULFID 130 154
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 297 330
 FT DISULFID 376 442
 FT DISULFID 383 415
 FT CARBOHYD 87 87
 FT CARBOHYD 137 137
 FT CARBOHYD 144 144
 FT CARBOHYD 153 153
 FT CARBOHYD 157 157
 FT CARBOHYD 185 185
 FT CARBOHYD 188 188
 FT CARBOHYD 198 198
 FT CARBOHYD 235 235
 FT CARBOHYD 242 242
 FT CARBOHYD 263 263
 FT CARBOHYD 277 277
 FT CARBOHYD 290 290
 FT CARBOHYD 331 331
 FT CARBOHYD 338 338
 FT CARBOHYD 353 353
 FT CARBOHYD 384 384
 FT CARBOHYD 390 390
 FT CARBOHYD 402 402
 FT CARBOHYD 441 441
 FT CARBOHYD 445 445
 FT CARBOHYD 458 458
 FT CARBOHYD 459 459
 FT CARBOHYD 462 462
 FT CARBOHYD 608 608
 FT CARBOHYD 613 613
 FT CARBOHYD 622 622
 FT CARBOHYD 634 634
 FT CARBOHYD 671 671
 SQ SEQUENCE 853 AA; 97043 MW; 849B08CBAFF7008 CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 853;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 DB 659 ELDKWA 664
 RESULT 14
 ID ENV_HV1A2 STANDARD; PRT; 855 AA.
 AC P03378;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV
 UN HIV immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).

FT	CHAIN	30	509	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	510	855	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	210	BY SIMILARITY.
FT	DISULFID	125	201	BY SIMILARITY.
FT	DISULFID	130	162	BY SIMILARITY.
FT	DISULFID	223	252	BY SIMILARITY.
FT	DISULFID	233	244	BY SIMILARITY.
FT	DISULFID	301	335	BY SIMILARITY.
FT	DISULFID	381	442	BY SIMILARITY.
FT	DISULFID	388	415	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	145	145	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	165	165	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	192	192	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	192	192	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	246	246	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	267	267	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	281	281	N-LINKED (GLCNAC. . .) (POTENTIAL) .

[illegible]

Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 662 ELDKWA 667

RESULT 18

ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS virus";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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CC EMBL; K03455; AAB50262.1; --
DR EMBL; AF038399; AAB99976.1; --
DR EMBL; AF03819; AAC82596.1; --
DR PDB; 1DF4; 26-JAN-00.
DR PDB; 1DF5; 26-JAN-00.
DR PDB; 1DL8; 02-APR-00.
DR PDB; 1G9M; 27-DEC-00.
DR PDB; 1GCI; 19-AUG-98.
DR PDB; 1GZL; 10-OCT-02.
DR PDB; 1K33; 10-OCT-01.
DR PDB; 1K34; 10-OCT-01.
DR HIV; K03455; ENVSHXB2.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR00777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 31 511 TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 BY SIMILARITY.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.

FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97212 MW; 6FABI6AF85107F80 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 856;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 662 ELDKWA 667

RESULT 19

ENV_HV1H3 STANDARD; PRT; 856 AA.
AC P04524;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11707;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85228248; PubMed=2988795;
RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;
RT "HTLV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";
RL Cell 41:979-986(1985).
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CC EMBL; M14100; AAA44679.1; --

FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 357 357 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 467 467 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 618 618 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 639 639 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 819 819 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 859 AA; 97109 MW; DBCF9AAS2E3ABF29 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 859;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 664 ELDKWA 669

RESULT 26
ENV_HVIRH STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentiviridae.
OX NCBI_TaxID=11686;
RN [1]
RP MEDLINE=85099333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Dancos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).
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CC -----
CC EMBL; K02013; AAB59751.1; -;
DR EMBL; A04321; CAA00352.1; -;
DR PIR; A03975; VCLJLV
DR FDB; IERF; 20-FEB-02.
DR HIV; K02013; ENV\$BRU.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal;
3D-structure. 1 30
FT SIGNAL 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 861 TRANSMEMBRANE GLYCOPROTEIN.
FT

FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 210 BY SIMILARITY.
FT DISULFID 126 201 BY SIMILARITY.
FT DISULFID 131 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 233 244 BY SIMILARITY.
FT DISULFID 301 336 BY SIMILARITY.
FT DISULFID 383 450 BY SIMILARITY.
FT DISULFID 390 423 BY SIMILARITY.
FT CARBOHYD 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 630 630 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 755 755 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 821 821 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4FD63A CRC64;

Query Match 100.0%; Score 35; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 667 ELDKWA 672

RESULT 27
ENV_HVIRH STANDARD; PRT; 865 AA.
AC P04579;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentiviridae.
OX NCBI_TaxID=11701;
RN [1]
RP MEDLINE=86218077; PubMed=2423250;
RX Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal P.;
RT "Identification and characterization of conserved and variable
regions in the envelope gene of HTLV-III/LAV, the retrovirus of
AIDS.";
RT


```
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD binding 1; 1.
DR Pfam; PF00174; oxidored molyb; 1.
DR PRINTS; PR00406; CYBSRDTASE.
DR PRINTS; PR00363; CYTOCHROMEBS.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PRODOM; PD000612; Cyt B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS02255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation.
FT METAL 204 204 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 258 258 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 443 443 INTERCHAIN (POTENTIAL).
FT METAL 586 586 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 609 609 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 303 303 D -> A (IN REF. 2).
SQ SEQUENCE 926 AA; 103970 MW; FF21DF01963F1AFC CRC64;

Query Match 100.0%; Score 35; DB 1; Length 926;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 845 ELDKWA 850

RESULT 29
Y067 CHLTR
ID Y067 CHLTR STANDARD; PRT; 326 AA.
AC Q95529; O84070;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative metal-binding lipoprotein CTO67 precursor.
GN CTO67.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2/434/Bu;
RX MEDLINE=99392470; PubMed=10463174;
RA Bannantine J.P., Rockey D.D.;
RT "Use of primate model system to identify Chlamydia trachomatis protein
RT antigens recognized uniquely in the context of infection.";
RL Microbiology 145:2077-2085(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=9900809; PubMed=9784136;
RA Stephens R.S., Kallan S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -1- FUNCTION: PART OF AN ATP-DRIVEN TRANSPORT SYSTEM
CC CTO67/CTO68/CTO69/CTO70 FOR A METAL. METAL-BINDING COMPONENT.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Probable).
CC -1- SIMILARITY: Belongs to the bacterial solute-binding protein family
CC 9.
CC
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CC EMBL; AF077010; AAC35948.1; ALT_INIT.
CC EMBL; AE001281; AAC67658.1; -.
DR PIR; E71561; E71561.
DR FIC1-2DPAGE; Q98529; -.
DR InterPro; IPR006128; Lipoprotein_4.
DR InterPro; IPR006127; SBP_bac_9.
DR Pfam; PF01297; SBP_bac_9; 1.
DR PRINTS; PR00690; ADHESINFAMILY.
KW Hypothetical protein; Transport; Metal-binding; Lipoprotein; Membrane;
KW Signal; Complete proteome; Palmitate.
FT SIGNAL 1 21 PROBABLE.
FT CHAIN 22 326 PUTATIVE METAL-BINDING LIPOPROTEIN
CT067.
FT LIPID 22 22 N-palmitoyl cysteine (Probable).
FT LIPID 22 22 S-diacylglycerol cysteine (Probable).
FT VARIANT 190 190 A -> V (IN SEROVAR L2).
SQ SEQUENCE 326 AA; 37035 MW; 5ASAA35AB6627D89 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 326;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 184 ELDRWA 189

RESULT 30
LGT_TREPA
ID LGT_TREPA STANDARD; PRT; 332 AA.
AC O83824;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-).
GN LGT OR TP0852.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -1- FUNCTION: Transfers the N-acyl diglyceride group on what will
CC become the N-terminal cysteine of membrane lipoproteins.
CC -1- PATHWAY: Lipoproteins biosynthesis; first step.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: Belongs to the lgt family.
CC
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EMBL; AE001255; AAC65817.1; -.

PIR; D71274; D71274.

TIGR; TP0852; -.

InterPro; IPR001640; LGT.

DR Pfam; PF01790; LGT; 1.
 DR ProDom; PD005412; LGT; 1.
 DR TIGRFAMs; TIGR00544; LGT; 1.
 DR PROSITE; PS01311; LGT; 1.
 KW Transferase; Transmembrane; Inner membrane; Complete proteome.
 FT TRANSFERASE 19 39 POTENTIAL.
 FT TRANSMEM 66 86 POTENTIAL.
 FT TRANSMEM 111 131 POTENTIAL.
 FT TRANSMEM 172 192 POTENTIAL.
 FT TRANSMEM 221 241 POTENTIAL.
 FT TRANSMEM 249 269 POTENTIAL.
 FT TRANSMEM 302 322 POTENTIAL.
 SQ SEQUENCE 332 AA; 38154 MW; 6FD260564892269D CRC64;

Query Match 91.4%; Score 32; DB 1; Length 332;

Best Local Similarity 83.3%; Pred. No. 31;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6

|||||
 47 ELDKWS 52

RESULT 31

ID T2S1 STRAH STANDARD; PRT; 358 AA.

AC O31074;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Type II restriction enzyme SacI (EC 3.1.21.4) (Endonuclease SacI)

DE (R.SacI).

GN SACIR.

OS Streptomyces achromogenes.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomycetes.

OX NCBI_TaxID=67255;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 12767;

RX MEDLINE=99077292; PubMed=9862476;

RA Xu S.-Y., Xiao J.-P., Ettwiller L., Holden M., Aliotta J., Poh C.L.,

RA Dalton M., Robinson D.P., Petronzio T.R., Moran L., Ganatra M.,

RA Ware J., Slatko B., Benner J. II;

RT "Cloning and expression of the ApaLI, NspI, NspHI, SacI, ScaI, and

RT SspI restriction-modification systems in *Escherichia coli*."

RL Mol. Gen. Genet. 260:226-231(1998).

CC -1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GAGCTC AND

CC CLEAVES AFTER T-5.

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give

CC specific double-stranded fragments with terminal 5'-phosphates.

CC -----

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CC -----

DR EMBL; AF027867; AAC97119.1; -.

KW REBASE; 1578; SacI.

SQ SEQUENCE 358 AA; 39965 MW; EBF68CB8037EBF13 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 358;

Best Local Similarity 83.3%; Pred. No. 34;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6

|||||
 347 ELDRWA 352

RESULT 32

NIAI MAIZE

ID NIAI MAIZE STANDARD; PRT; 621 AA.

AC P17571;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. W64 X W128E; TISSUE=Leaf;

RA Gowri G., Campbell W.H.;

RT "cDNA clones for corn leaf NADH: nitrate reductase and chloroplast

RT NAD(P) (+): glyceraldehyde-3-phosphate dehydrogenase.";

RL Plant Physiol. 90:792-798(1989).

RN [2]

RP REVISIONS TO 389-390; 405-406 AND 414-417, AND CHARACTERIZATION.

RC STRAIN=cv. W64 X W128E; TISSUE=Leaf;

RX MEDLINE=90267474; PubMed=2189408;

RA Hyde G.E., Campbell W.H.;

RT "High-level expression in *Escherichia coli* of the catalytically

RT active flavin domain of corn leaf NADH:nitrate reductase and its

RT comparison to human NADH:cytochrome B5 reductase.";

RL Biochem. Biophys. Res. Commun. 168:1285-1291(1990).

RN [3]

RP SECONDARY STRUCTURE OF FAD DOMAIN.

RX MEDLINE=92084635; PubMed=1748631;

RA Hyde G.E., Crawford N.M., Campbell W.H.;

RT "The sequence of squash NADH:nitrate reductase and its relationship

RT to the sequences of other flavoprotein oxidoreductases. A family of

RT flavoprotein pyridine nucleotide cytochrome b reductases.";

RL J. Biol. Chem. 266:23542-23547(1991).

RN [4]

RP MUTAGENESIS OF CYS-593.

RX MEDLINE=94245686; PubMed=8188655;

RA Dwivedi U.N., Shiraishi N., Campbell W.H.;

RT "Identification of an 'essential' cysteine of nitrate reductase via

RT mutagenesis of its reconstituted cytochrome b reductase domain.";

RL J. Biol. Chem. 269:13785-13791(1994).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF FAD DOMAIN.

RX MEDLINE=95111952; PubMed=7812715;

RA Lu G., Campbell W.H., Schneider G., Lindqvist Y.;

RT "Crystal structure of the FAD-containing fragment of corn nitrate

RT reductase at 2.5-A resolution: relationship to other flavoprotein

RT reductases.";

RL Structure 2:809-821(1994).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 232-501.

RX MEDLINE=95280311; PubMed=7760334;

RA Lu G., Lindqvist Y., Schneider G., Dwivedi U., Campbell W.H.;

RT "Structural studies on corn nitrate reductase: refined structure of

RT the cytochrome b reductase fragment at 2.5 A, its ADP complex and an

RT active-site mutant and modeling of the cytochrome b domain.";

RL J. Mol. Biol. 248:931-948(1995).

CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first

CC step of nitrate assimilation in plants, fungi and bacteria.

CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.

CC -1- COFACTOR: Requires FAD, a heme group (called cytochrome b-557) and

CC one molybdenum atom.

CC -1- SUBUNIT: Homodimer.

CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE

CC N-TERMINAL DOMAIN.

CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.

CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE

CC C-TERMINAL DOMAIN.

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CC or send an email to license@sib-sib.ch).

Entity	Residue	Sequence	Function
ENBL	M27821	AAA03202.1; ALT_SEQ.	
PDB	2CND	20-APR-95.	
PDB	1CNE	20-APR-95.	
PDB	1CNF	20-APR-95.	
MaizeDB	25899	-	
DR	InterPro	IPR001199; Cyt B5.	
DR	InterPro	IPR001834; Cyt_B5_reductase.	
DR	InterPro	IPR008335; Euk_Mb_oxred.	
DR	InterPro	IPR008333; FAD_binding_6.	
DR	InterPro	IPR001709; FPN_cyt_redctse.	
DR	InterPro	IPR007110; Ig-Like.	
DR	InterPro	IPR005066; Mo-co_dimer.	
DR	InterPro	IPR000572; Oxidized_molyb.	
DR	InterPro	IPR001433; Oxred_FAD/NAD(P).	
DR	Pfam	PF00970; FAD_binding_6; 1.	
DR	Pfam	PF00173; heme_1; 1.	
DR	Pfam	PF03404; Mo-co_dimer; 1.	
DR	Pfam	PF00175; NAD_binding_1; 1.	
DR	Pfam	PF00174; oxidized_molyb; 1.	
DR	PRINTS	PR00406; CYTBSRDTASE.	
DR	PRINTS	PR00363; CYTOCHROME_B5.	
DR	PRINTS	PR00407; EUMOPTERIN.	
DR	PRINTS	PR00371; FPNCR.	
DR	ProDom	PD000612; Cyt B5; 1.	
DR	PROSITE	PS00191; CYTOCHROME_B5_1; 1.	
DR	PROSITE	PS02555; CYTOCHROME_B5_2; 1.	
DR	PROSITE	PS00559; MOLYBDOPTERIN_EUK; PARTIAL.	
DR	PROSITE	PS00559; MOLYBDOPTERIN_EUK; PARTIAL.	
KW	Nitrate reductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;		
KW	Nitrate assimilation; Multigene family; 3D-structure.		
FT	NON TER	1	
FT	DUF127	138	
FT	METAL	284	
FT	METAL	307	
FT	SITE	593	
FT	MUTAGEN	593	
FT	STRAND	364	
FT	TURN	376	
FT	STRAND	378	
FT	TURN	388	
FT	TURN	396	
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FT	TURN	421	
FT	STRAND	426	
FT	STRAND	439	
FT	TURN	440	
FT	STRAND	442	
FT	TURN	443	
FT	HELEX	447	
FT	TURN	457	
FT	STRAND	460	
FT	STRAND	470	
FT	STRAND	478	
FT	TURN	481	
FT	STRAND	483	
FT	STRAND	489	
FT	HELEX	496	
FT	HELEX	499	
FT	TURN	512	
FT	STRAND	519	
FT	HELEX	529	
FT	TURN	533	
FT	HELEX	535	

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FT DISULFID 388 452 BY SIMILARITY.
FT DISULFID 395 425 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 87 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 136 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 623 623 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 863 AA; 97743 MW; B729CB5A6FAD1641 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 863;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 669 QLDKWA 674

RESULT 34
ENV_HV1C4
ID ENV_HV1C4 STANDARD; PRT; 868 AA.
AC P05879;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP11)].
GN ENV.
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11687;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041461; PubMed=3490666;
RA Desai S.M., Kalyanaram V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384 (1986).
RN [2]
RP SEQUENCE OF 34-43.
RX MEDLINE=90253924; PubMed=2187500;
RA Kalyanaram V.S., Rodriguez V., Veronese F., Rahman R., Lusso P.,
RA DeVico A.L., Copeland T., Oroszian S., Gallo R.C., Sarngadharan M.G.;
RT "Characterization of the secreted, native gp120 and gp160 of the human
RT immunodeficiency virus type 1.";

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RL AIDS Res. Hum. Retroviruses 6:371-380 (1990).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M13137; AAA44311.1; -.
DR PIR; C25523; VCLJH4.
DR HIV; M13137; ENV$CD045.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 33
FT CHAIN 34 522 EXTERIOR MEMBRANE GLYCOPROTEIN (GP120).
FT CHAIN 523 868 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 55 75 BY SIMILARITY.
FT DISULFID 120 216 BY SIMILARITY.
FT DISULFID 127 207 BY SIMILARITY.
FT DISULFID 132 163 BY SIMILARITY.
FT DISULFID 229 258 BY SIMILARITY.
FT DISULFID 239 250 BY SIMILARITY.
FT DISULFID 307 341 BY SIMILARITY.
FT DISULFID 387 456 BY SIMILARITY.
FT DISULFID 394 429 BY SIMILARITY.
FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 459 459 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 628 628 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 828 828 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 868 AA; 98698 MW; A11527FC52A6F0C8 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 84;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 674 QLDKWA 679

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RESULT 35
NIA3_MAIZE
ID NIA3_MAIZE STANDARD; PRT; 889 AA.
AC P49102;
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 3 (EC 1.7.1.1) (NR).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. B73; TISSUE=Seedling;
RA Campbell W.H., Redinbaugh M.G., Ingemarsson B., Dougherty E.S.,
RA Campbell E.R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557 (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
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CC -----
CC EMBL; U20450; AAA62316.1; -.
CC PIR; T02240; T02240.
CC DR HSSP; P17571; 2CND.
CC DR MaizeDB; 30041; -.
CC DR InterPro; IPR001199; Cyt_B5.
CC DR InterPro; IPR001834; Cyt_B5_reductase.
CC DR InterPro; IPR008335; Euk_Mb_oxred.
CC DR InterPro; IPR008333; FAD_binding_6.
CC DR InterPro; IPR001709; FPN_cyt_redctse.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR005066; Mo-co_dimer.
CC DR InterPro; IPR000572; Oxidored_molyb.
CC DR InterPro; IPR001433; Oxred_FAD/NAD(P).
CC DR InterPro; IPR001221; Phe_hydroxylase.
CC DR Pfam; PF00970; FAD_binding_6; 1.
CC DR Pfam; PF00173; heme_1; 1.
CC DR Pfam; PF03404; Mo-co_dimer; 1.
CC DR Pfam; PF00175; NAD_binding_1; 1.
CC DR Pfam; PF00174; oxidored_molyb; 1.
CC DR PRINTS; PR00406; CYTB5RDTASE.
CC DR PRINTS; PR00363; CYTOCHROME B5.
CC DR PRINTS; PR00407; EUMOPTERIN.
CC DR PRINTS; PR00371; FPNCR.
CC DR PRINTS; PR00410; PHEHYDRLASE.
CC DR ProDom; PD000612; Cyt_B5; 1.
CC DR PROSITE; PS00191; CYTOCHROME B5 1; 1.
CC DR PROSITE; PS00255; CYTOCHROME B5 2; 1.
CC DR PROSITE; PS00559; MOLYBDOPTERIN EUK; 1.
CC DR Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
KW METAL 181
KW METAL 235 MOLYBDENUM-PTERIN (POTENTIAL).
KW METAL 235 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 235 235
FT DISULFID 404 404 INTERCHAIN (POTENTIAL).

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FT METAL 555 555 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 578 578 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 889 AA; 98811 NW; 3614A8BB44B822F5 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 889;
Best Local Similarity 83.3%; Pred. NO. 86;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 806 ELDRWA 811
|||:|
|||:|

RESULT 36
NIA2_HORVU
ID NIA2_HORVU STANDARD; PRT; 912 AA.
AC P27959;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR) (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Steptoe; TISSUE=Leaf;
RX MEDLINE=91326031; PubMed=1865878;
RA Schnorr K.M., Juricek M., Huang C., Culley D., Kleinhofs A.;
RT "Analysis of barley nitrate reductase cDNA and genomic clones.";
RL Mol. Gen. Genet. 227:411-416(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X57844; CAA40975.1; -.
CC PIR; S17454; RDBHNS.
CC DR HSSP; P17571; 2CND.
CC DR InterPro; IPR001199; Cyt_B5.
CC DR InterPro; IPR001834; Cyt_B5_reductase.
CC DR InterPro; IPR008335; Euk_Mb_oxred.
CC DR InterPro; IPR008333; FAD_binding_6.
CC DR InterPro; IPR001709; FPN_cyt_redctse.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR005066; Mo-co_dimer.
CC DR InterPro; IPR000572; Oxidored_molyb.
CC DR InterPro; IPR001433; Oxred_FAD/NAD(P).
CC DR Pfam; PF00970; FAD_binding_6; 1.
CC DR Pfam; PF00173; heme_1; 1.
CC DR Pfam; PF03404; Mo-co_dimer; 1.
CC DR Pfam; PF00175; NAD_binding_1; 1.
CC DR Pfam; PF00174; oxidored_molyb; 1.
CC DR PRINTS; PR00406; CYTB5RDTASE.
CC DR PRINTS; PR00363; CYTOCHROME B5.

```

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DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PR0Dom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
DR OXidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT NON TER 1
FT METAL 186 186 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 240 240 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 425 425 INTERCHAIN (POTENTIAL).
FT METAL 570 570 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 593 593 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 912 AA; 101467 MW; 47AB9C5B303190CC CRC64;

Query Match 91.4%; Score 32; DB 1; Length 912;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 828 ELDRWA 833

RESULT 37
NIAL HORVU
ID NIAL HORVU STANDARD; PRT; 915 AA.
AC P27967;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] (EC 1.7.1.1) (NR).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Himalaya; TISSUE=Leaf;
RX MEDLINE=91326031; PubMed=1865878;
RA Schnorr K.M., Juricek M., Huang C., Culley D., Kleinhofs A.;
RT "Analysis of barley nitrate reductase cDNA and genomic clones.";
RL Mol. Gen. Genet. 227:411-416(1991).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; X57845; CAA40976.1; -.
CC PIR; S17453; RDBHNF.
CC HSSP; P17571; 2GND.
CC InterPro; IPR001199; Cyt_B5.
CC InterPro; IPR001834; Cyt_B5_reductase.
CC InterPro; IPR008335; Euk_Mb_oxred.
CC InterPro; IPR008333; FAD_Binding_6.

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DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR005066; MO-co dimer.
DR InterPro; IPR000572; Oxidored molyb.
DR InterPro; IPR001433; Oxred FAD/NAD(P).
DR Pfam; PF00970; FAD_binding_6; 1.
DR Pfam; PF00173; heme_1; 1.
DR Pfam; PF03404; Mo-co dimer; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF00174; oxidored molyb; 1.
DR PRINTS; PR00406; CYTB5RDTASE.
DR PRINTS; PR00363; CYTOCHROME B5.
DR PRINTS; PR00407; EUMOPTERIN.
DR PRINTS; PR00371; FPNCR.
DR PR0Dom; PD000612; Cyt_B5; 1.
DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
DR PROSITE; PS0255; CYTOCHROME B5_2; 1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
KW Nitrate assimilation; Multigene family.
FT METAL 189 189 MOLYBDENUM-PTERIN (POTENTIAL).
FT METAL 243 243 MOLYBDENUM-PTERIN (POTENTIAL).
FT DISULFID 428 428 INTERCHAIN (POTENTIAL).
FT METAL 573 573 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 596 596 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 915 AA; 101770 MW; 937FFA9686FDA56 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 915;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 831 ELDRWA 836

RESULT 38
NIAL ORYSA
ID NIAL ORYSA STANDARD; PRT; 916 AA.
AC P16081;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1).
GN NIAL.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M201;
RX MEDLINE=91370859; PubMed=2491689;
RA Cheng C., Dewdney J., Nam H., den Boer B.G.W., Goodman H.M.,
RA Choi H.K., Kleinhofs A., An G.;
RT "Nucleotide sequence of rice nitrate reductase genes.";
RL Plant Mol. Biol. 13:731-733(1989).
CC -1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
CC step of nitrate assimilation in plants, fungi and bacteria.
CC -1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
CC -1- COFACTOR: Each subunit of the enzyme contains 1 equivalent of FAD,
CC heme iron, and molybdenum-pterin as prosthetic groups. The heme
CC group is called cytochrome b-557.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
CC N-TERMINAL DOMAIN.
CC -1- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC -1- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
CC C-TERMINAL DOMAIN.
CC -----
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CC	the European Bioinformatics Institute. There are no restrictions on its	RT	"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
CC	use by non-profit institutions as long as its content is in no way	RT	features of the regions of 4,504,864 bp covered by sixty P1 and TAC
CC	modified and this statement is not removed. Usage by and for commercial	RT	clones";
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/	RL	DNA Res. 7:131-135(2000).
CC	or send an email to license@isb-sib.ch).	CC	-I- FUNCTION: This magnesium-dependent enzyme catalyzes the hydrolysis
DR	EMBL; X15819; CAA33817.2; -	CC	of ATP coupled with the translocation of calcium from the cytosol
DR	EMBL; X15820; CAA33817.2; JOINED.	CC	out of the cell or into organelles (By similarity).
DR	PIR; S07554; S07554.	CC	-I- CATALYTIC ACTIVITY: ATP + H(2)O + Ca(2+) (Cis) = ADP + phosphate +
DR	HSSP; P17571; 2CND.	CC	Ca(2+); (Trans).
DR	Gramene; P16081; -	CC	-I- ENZYME REGULATION: Activated by calmodulin (By similarity).
DR	InterPro; IPR001199; Cyt B5.	CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
DR	InterPro; IPR001834; Cyt_B5_reductase.	CC	-I- DOMAIN: The N-terminus contains an autoinhibitory calmodulin-
DR	InterPro; IPR008335; Cyt_Mb-oxred.	CC	binding domain, which binds calmodulin in a calcium-dependent
DR	InterPro; IPR008333; FAD_binding_6.	CC	fashion (By similarity).
DR	InterPro; IPR001709; FEN_cyt_redctse.	CC	-I- SIMILARITY: Belongs to the cation transport ATPases family (P-type
DR	InterPro; IPR007110; Ig-like.	CC	ATPases). Subfamily IIB.
DR	InterPro; IPR005066; Mo-co_dimer.	CC	-----
DR	InterPro; IPR000572; Oxidored_molylb.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
DR	InterPro; IPR001433; Oxred_FAD/NAD(P).	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
DR	InterPro; IPR001221; Phe_hydroxylase.	CC	the European Bioinformatics Institute. There are no restrictions on its
DR	Pfam; PF00970; FAD_binding_6; 1.	CC	use by non-profit institutions as long as its content is in no way
DR	Pfam; PF00173; heme_1; 1.	CC	modified and this statement is not removed. Usage by and for commercial
DR	Pfam; PF03404; Mo-co_dimer; 1.	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
DR	Pfam; PF00175; NAD_binding_1; 1.	CC	or send an email to license@isb-sib.ch).
DR	Pfam; PF00174; oxidored_molylb; 1.	CC	-----
DR	PRINTS; PR00406; CYTB5RDTASE.	DR	EMBL; AB023045; BAB01709.1; -
DR	PRINTS; PR00363; CYTOCHROMEBS.	DR	HSSP; P04191; IEUL.
DR	PRINTS; PR00407; EUMOPTERIN.	DR	InterPro; IPR006408; ATPase-IIB_Ca.
DR	PRINTS; PR00371; FPNCR.	DR	InterPro; IPR001757; ATPase_E1-E2.
DR	PRINTS; PR00410; PHEHYDRXKLASE.	DR	InterPro; IPR006068; Cation_ATPase_C.
DR	PRODOM; PR000612; Cyt_B5; 1.	DR	InterPro; IPR004014; Cation_ATPase_N.
DR	PROSITE; PS00191; CYTOCHROME_B5_1; 1.	DR	InterPro; IPR008250; E1-E2_ATPase_reg.
DR	PROSITE; PS02555; CYTOCHROME_B5_2; 1.	DR	InterPro; IPR005834; Hydrolase.
DR	PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.	DR	InterPro; IPR00689; Cation_ATPase_C; 1.
KW	Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;	DR	Pfam; PF00690; Cation_ATPase_N; 1.
KW	Nitrate assimilation; Multigene family.	DR	Pfam; PF00122; E1-E2_ATPase; 1.
FT	METAL 192 192 MOLYBDENUM-PTERIN (POTENTIAL).	DR	Pfam; PF00702; Hydrolase; 1.
FT	METAL 246 246 MOLYBDENUM-PTERIN (POTENTIAL).	DR	PRINTS; PR00119; CATATPASE.
FT	DISULFID 431 431 INTERCHAIN (POTENTIAL).	DR	TIGRFAMS; TIGR01517; ATPase-IIB_Ca; 1.
FT	METAL 576 576 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).	DR	TIGRFAMS; TIGR01494; ATPase_P-type; 5.
FT	METAL 599 599 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).	DR	PROSITE; PS00154; ATPase_E1-E2; 1.
SQ	SEQUENCE 916 AA; 101482 MW; BE97DA33E1DEAEC9 CRC64;	KW	Hydrolase; Calcium transport; Transmembrane; Phosphorylation;
		KW	ATP-binding; Metal-binding; Magnesium; Calmodulin-binding;
		KW	Multigene family; Hypothetical protein.
		FT	DOMAIN 1 181 CYTOPLASMIC (POTENTIAL).
		FT	TRANSEM 182 202 POTENTIAL.
		FT	DOMAIN 203 220 LUMENAL (POTENTIAL).
		FT	TRANSEM 221 241 POTENTIAL.
		FT	DOMAIN 242 369 CYTOPLASMIC (POTENTIAL).
		FT	TRANSEM 370 389 POTENTIAL.
		FT	DOMAIN 390 426 LUMENAL (POTENTIAL).
		FT	TRANSEM 427 444 POTENTIAL.
		FT	DOMAIN 445 844 CYTOPLASMIC (POTENTIAL).
		FT	TRANSEM 845 863 POTENTIAL.
		FT	DOMAIN 864 874 LUMENAL (POTENTIAL).
		FT	TRANSEM 875 895 POTENTIAL.
		FT	DOMAIN 896 915 CYTOPLASMIC (POTENTIAL).
		FT	TRANSEM 916 938 POTENTIAL.
		FT	DOMAIN 939 950 LUMENAL (POTENTIAL).
		FT	TRANSEM 951 975 POTENTIAL.
		FT	DOMAIN 976 993 CYTOPLASMIC (POTENTIAL).
		FT	TRANSEM 994 1015 POTENTIAL.
		FT	DOMAIN 1016 1025 LUMENAL (POTENTIAL).
		FT	TRANSEM 1026 1047 POTENTIAL.
		FT	DOMAIN 1048 1073 CYTOPLASMIC (POTENTIAL).
		FT	TRANSEM 1074 1088 CALMODULIN-BINDING (BY SIMILARITY).
		FT	DOMAIN 44 55 PHOSPHORYLATION (BY SIMILARITY).
		FT	MOD RES 482 482 MAGNESIUM (BY SIMILARITY).
		FT	METAL 789 789 MAGNESIUM (BY SIMILARITY).
		FT	METAL 793 793 MAGNESIUM (BY SIMILARITY).
		SQ	SEQUENCE 1073 AA; 117488 MW; 5AF6220EBD908069 CRC64;
			Query Match 91.4%; Score 32; DB 1; Length 1073;
			Best Local Similarity 83.3%; Pred. No. 89;
			Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 ELDKWA 6		
Db	832 ELDRWA 837		
RESULT 39			
ACA9 ARATH			
ID ACA9 ARATH	STANDARD; PRT; 1073 AA.		
AC Q9L041;			
DT 16-OCT-2001 (Rel. 40, Created)			
DT 16-OCT-2001 (Rel. 40, Last sequence update)			
DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DE Potential calcium-transporting ATPase 9, plasma membrane-type			
DE (EC 3.6.3.8) (Ca(2+)-ATPase isoform 9).			
GN ACA9 OR AT3G21180 OR MXL8.3.			
OS Arabidopsis thaliana (Mouse-ear cress).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
OX NCBI_TaxID=3702;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=cv. Columbia;			
RX MEDLINE=20277480; PubMed=10819329;			
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;			

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
:|||||
Db 665 DLDKWA 670

RESULT 40

YAFU_ECOLI
ID YAFU_ECOLI STANDARD; PRT; 112 AA.
AC P77354;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yafu.
GN YAFU OR B0218.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
RA Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
RA Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
RA Davis R.W.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC
CC -----
DR EMBL; AE000130; AAC73322.1; -;
DR EMBL; U70214; AAB08640.1; -;
DR PIR; C64746; C64746.
DR EcoGene; EG13333; yafu.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
SQ SEQUENCE 112 AA; 12136 MW; 78BE901E02429F0D CRC64;

Query Match 88.6%; Score 31; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 5
:|||||
Db 90 ELDKWA 94

RESULT 41

YAFU_ECOLI
ID YAFU_ECOLI STANDARD; PRT; 151 AA.
AC OXEWL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein yafu.

GN YAFU OR STM0397 OR STY0420 OR T2477.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2";
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18";
RL Nature 413:848-852(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyavani V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- SIMILARITY: Belongs to the UPF0178 family.
CC
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CC
CC -----
DR EMBL; AE008713; AAL19341.1; -;
DR EMBL; AL627266; CAD08842.1; -;
DR EMBL; AE016842; AA070065.1; -;
DR styGene; SG77777; yafu.
DR HAMAP; MF 00489; -; 1.
DR InterPro; IPR003791; DUF188.
DR Pfam; PF02639; DUF188; 1.
DR ProDom; PD016319; DUF188; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 151 AA; 16945 MW; F94F40A401EA753B CRC64;

Query Match 88.6%; Score 31; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 5
:|||||
Db 139 ELDKWA 143

RESULT 42

YU33 YERPE STANDARD; PRT; 152 AA.
AC Q8ZCF8; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0178 protein YP03033/Y1450.
GN YP03033 OR Y1450.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RA "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RA "Genome sequence of Yersinia pestis KIM.";
RT J. Bacteriol. 184:4601-4611(2002).
RL [1- SIMILARITY: Belongs to the UPF0178 family.
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CC
DR EMBL; AJ414155; CAC92275.1; -;
DR EMBL; AE013748; AAM85021.1; -;
DR PIR; AH0368; AH0368.
DR HAMAP; MF 00489; -; 1.
DR InterPro; IPR003791; DUF188.
DR Pfam; PF02639; DUF188; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 152 AA; 17096 MW; E173AAF49D1BF176 CRC64;
Query Match 88.6%; Score 31; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKW 5
DB 139 ELDKW 143
RESULT 43
DHB2 MOUSE STANDARD; PRT; 381 AA.
AC P51658; O08898;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Estradiol 17 beta-dehydrogenase 2 (EC 1.1.1.62) (17-beta-HSD 2)
DE (17-beta-hydroxysteroid dehydrogenase 2).

GN HSD17B2 OR EDH17B2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=973444259; PubMed=9224647;
RA Mustonen M.;
RT "Cloning of mouse 17beta-hydroxysteroid dehydrogenase type 2, and
RT analysys and adult tissues.";
RL Biochem. J. 325:199-205(1997).
RN [2]
RP SEQUENCE OF 1-358 FROM N.A.
RC STRAIN=BALB/c;
RX Scofield W., Weiss B.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CAPABLE OF CATALYZING THE INTERCONVERSION OF
CC TESTOSTERONE AND ANDROSTENEDIONE, AS WELL AS ESTRADIOL AND
CC ESTRONE. ALSO HAS 20-ALPHA-HSD ACTIVITY. USES NADH WHILE EDH17B3
CC USES NADPH (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Estradiol-17-beta + NAD(P) (+) = estrone +
CC NAD(P)H.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC
DR EMBL; Y09517; CAA70706.1; -;
DR EMBL; X95685; CAA64982.1; -;
DR HSP; P14061; 1FPU.
DR MGD; MGI:1096386; Hsd17b2.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Steroid biosynthesis; Oxidoreductase; NAD; Multigene family;
KW Transmembrane; Signal-anchor
TRANSMEM 4 24 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT NP_BIND 83 112 NAD (BY SIMILARITY).
FT ACT_SITE 233 233 BY SIMILARITY.
FT CONFLICT 36 37 QA -> RP (IN REF. 2).
SQ SEQUENCE 381 AA; 41835 MW; 7AA62797947E6086 CRC64;
Query Match 88.6%; Score 31; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKW 5
DB 250 ELDKW 254
RESULT 44
GAG_HV1W2 STANDARD; PRT; 388 AA.
AC P05889;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polypeptide [Contains: Core proteins P17, P24, P2, P7, P1, P6]
DE (Fragment).
GN GAG.

```
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS.";
RL Science 232:1548-1553 (1986).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: The p24 protein is phosphorylated.
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K03457; AAB12988.1; -.
DR PDB; 1FGL; 01-APR-97.
DR HIV; K03457; GAG$WMJ2.
DR InterPro; IPR000721; Gag_p24.
DR InterPro; IPR008916; Retrov_capsid_C.
DR InterPro; IPR008919; Retrov_capsid_N.
DR InterPro; IPR000071; Retrov_p17.
DR Pfam; PF00540; Gag_p17; 1.
DR Pfam; PF00607; Gag_p24; 1.
DR PRINTS; PR00234; HIV1MATRIX.
KW AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
KW Zinc-finger; 3b-structure; Lipoprotein.
FT INIT MET 0 0 BY SIMILARITY.
FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 363 376 CORE PROTEIN P2.
FT CHAIN 377 >388 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT LIPID 1 1 N-myristoyl glycine (in host) (By
FT similarity).
FT NON TER 388 388
SQ SEQUENCE 388 AA; 43314 MW; EF895BE10ECF7804 CRC64;
Query Match 88.6%; Score 31; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKW 5
DB 11 ELDKW 15
RESULT 45
GALI_STRPN STANDARD; PRT; 392 AA.
AC Q97N26;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galactokinase (EC 2.7.1.6) (Galactose kinase).
GN GALK OR SP1853.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
```

```
OC Streptococcus.
OX NCBI_TaxID=13113;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Urkin A.S., White M., Kolonay J.F., Nelson M.C., Peterson J.D.,
RA Unayam L.A., Gwinn O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Ueberback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollinghead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506 (2001).
CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
CC phosphate.
CC -1- PATHWAY: Galactose metabolism; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: Belongs to the GHMP kinase family. GALK subfamily.
CC -----
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CC -----
DR EMBL; AE007477; AAK75925.1; -.
DR PIR; D95216; D95216.
DR TIGR; SP1853; -.
DR HAMAP; MF_00246; -.
DR InterPro; IPR000705; Galactokinase.
DR InterPro; IPR006204; GHMP_kinase.
DR InterPro; IPR006203; GHMPKnsse_ATP.
DR InterPro; IPR006206; Mv_galkinase.
DR Pfam; PF00288; GHMP_kinases; 1.
DR PRINTS; PR00473; GALKTOKINASE.
DR PRINTS; PR00959; MEVGALKINASE.
DR TIGRFAMS; TIGR00131; gal_kin; 1.
DR PROSITE; PS00106; GALKTOKINASE; 1.
DR PROSITE; PS00637; GHMP_KINASES_ATP; 1.
KW Transferase; Kinase; Galactose metabolism; ATP-binding;
KW Complete proteome.
FT NP BIND 126 136 ATP (POTENTIAL).
FT NP BIND 126 136
SQ SEQUENCE 392 AA; 43584 MW; 946034F1FEA50095 CRC64;
Query Match 88.6%; Score 31; DB 1; Length 392;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 253 ELDEWA 258
RESULT 46
GALI_STRRG STANDARD; PRT; 392 AA.
ID GAL1_STRRG
AC Q8DNK7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Galactokinase (EC 2.7.1.6) (Galactose kinase).
GN GALK OR SP1668.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
```

RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.B. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Garra M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.B., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Kosteck P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
CC phosphate.
CC -1- PATHWAY: Galactose metabolism; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the GHMP kinase family. Galk subfamily.
CC
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CC
CC EMBL; AE008532; ALU00471.1; -.
DR PIR; B98080; B98080.
DR HAMAP; MF 00246; -; 1.
DR InterPro; IPR000705; Galactokinase.
DR InterPro; IPR006203; GHMPkinase ATP.
DR InterPro; IPR006204; GHMP kinase.
DR InterPro; IPR006206; Mv_galkinase.
DR Pfam; PF00288; GHMP kinases; 1.
DR PRINTS; PR00473; GALCTOKINASE.
DR PRINTS; PR00959; MEVGALKINASE.
DR TIGRFS; TIGR00131; gal kin; 1.
DR PROSITE; PS00106; GALACTOKINASE; 1.
DR PROSITE; PS00627; GHMP KINASES_ATP; 1.
KW Transferase; Kinase; Galactose metabolism; ATP-binding;
KW Complete proteome.
FT NP BIND 126 136 ATP (POTENTIAL).
SQ SEQUENCE 392 AA; 43672 MW; 8503611AC5FCC394 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 392;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
Db 253 ELDEWA 258
|||||

RESULT 47
ECB2_HALEL
ID ECB2_HALEL STANDARD; PRT; 421 AA.
AC O52250;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Diaminobutyrate-pyruvate aminotransferase (EC 2.6.1.46) (L-
DE diaminobutyric acid transaminase) (Diaminobutyrate transaminase).
GN ECTB.
OS Halomonas elongata.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Halomonadaceae; Halomonas.
OX NCBI_TaxID=2746;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 2581T.
RX MEDLINE=98231640; PubMed=9570121;
RA Goller K., Ofer A., Galinski E.A.;

RT "Construction and characterization of an NaCl-sensitive mutant of
RT Halomonas elongata impaired in ectoine biosynthesis.";
RL FEMS Microbiol. Lett. 161:293-300(1998).
CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutanoate + pyruvate = L-
CC aspartate 4-semialdehyde + L-alanine.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Biosynthesis of ectoine (1,4,5,6-tetrahydro-2-methyl-4-
CC pyrimidine carboxylic acid); first step.
CC -1- SUBUNIT: Homohexamer (By similarity).
CC -1- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
CC
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CC
CC EMBL; AF031489; AAC15882.1; -.
DR HSP; P12995; IQJ3.
DR InterPro; IPR005814; Aminotrans_3.
DR InterPro; IPR004637; Dat.
DR Pfam; PF00202; aminotran_3; 1.
DR TIGRFS; TIGR00709; dat; 1.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; FALSE NEG.
KW Transferase; Aminotransferase; Pyridoxal phosphate.
FT BINDING 267 267 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 421 AA; 46166 MW; AA42E21596E1E16C CRC64;

Query Match 88.6%; Score 31; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5
Db 284 ELDKW 288
|||||

RESULT 48
GAG_HVIOY
ID GAG_HVIOY STANDARD; PRT; 498 AA.
AC P20889;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11699;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148544; PubMed=2559749;
RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
RT individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989)
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: The p24 protein is phosphorylated.
CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC HEALTHY GABONESE INDIVIDUAL.
CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
CC
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CC EMBL; M26727; AAA83391.1; -
 DR HSPF; P05888; IAAF.
 DR HIV; M26727; GAGSOYI.
 DR InterPro; IPR000721; Gag_p24.
 DR InterPro; IPR008916; Retrov capsid C.
 DR InterPro; IPR008919; Retrov capsid N.
 DR InterPro; IPR000071; Retrovir_p17.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00540; Gag_p17; 1.
 DR Pfam; PF00607; Gag_p24; 1.
 DR Pfam; PF00098; Zf_CCHC; 2.
 DR PRINTS; PR00234; HIVMATRIX.
 DR SMART; SM00343; Znf_C2HC; 2.
 DR PROSITE; PS0158; ZF_CCHC; 2.
 DR AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
 KW Zinc-finger; Repeat; Lipoprotein.
 KW INIT MET 0 BY SIMILARITY.
 FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 363 376 CORE PROTEIN P2.
 FT CHAIN 377 430 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 431 446 CORE PROTEIN P1.
 FT CHAIN 447 498 CORE PROTEIN P6.
 FT ZN_FING 388 405 CCHC-TYPE 1.
 FT ZN_FING 409 426 CCHC-TYPE 2.
 FT LIPID 1 1 N-myristoyl glycine (in host) (By similarity).
 SQ SEQUENCE 498 AA; 55451 MW; BDFP20658DEB20B1 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
 |||||
 Db 11 ELDKW 15

RESULT 49
 GAG_HV1N5
 ID GAG_HV1N5 STANDARD; PRT; 499 AA.
 AC P12493;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11698;
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE PNL4-3).
 RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
 RL Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: The p24 protein is phosphorylated.
 CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.

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CC EMBL; M19921; AAA44987.1; -
 DR PDB; 1A43; 09-FEB-99.
 DR PDB; 1A80; 28-OCT-97.
 DR PDB; 1AFV; 20-AUG-97.
 DR PDB; 1AK4; 15-OCT-97.
 DR PDB; 1AUM; 14-JAN-98.
 DR PDB; 1BAJ; 18-NOV-98.
 DR PDB; 1GDS; 30-DEC-96.
 DR PDB; 1GDY; 30-DEC-96.
 DR PDB; 1GDZ; 30-DEC-96.
 DR PDB; 1GWP; 21-JUN-02.
 DR HIV; M19921; GAGSNL43.
 DR InterPro; IPR000721; Gag_p24.
 DR InterPro; IPR008916; Retrov capsid C.
 DR InterPro; IPR008919; Retrov capsid N.
 DR InterPro; IPR000071; Retrovir_p17.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00540; Gag_p17; 1.
 DR Pfam; PF00607; Gag_p24; 1.
 DR Pfam; PF00098; Zf_CCHC; 2.
 DR PRINTS; PR00234; HIVMATRIX.
 DR SMART; SM00343; Znf_C2HC; 2.
 DR PROSITE; PS0158; ZF_CCHC; 2.
 DR AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
 KW Zinc-finger; Repeat; 3D-structure; Lipoprotein.
 KW INIT MET 0 BY SIMILARITY.
 FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 363 376 CORE PROTEIN P2.
 FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 432 447 CORE PROTEIN P1.
 FT CHAIN 448 499 CORE PROTEIN P6.
 FT ZN_FING 389 406 CCHC-TYPE 1.
 FT ZN_FING 410 427 CCHC-TYPE 2.
 FT LIPID 1 1 N-myristoyl glycine (in host) (By similarity).
 SQ SEQUENCE 499 AA; 55687 MW; C8ECC1302FE2C1E2 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKW 5
 |||||
 Db 11 ELDKW 15

RESULT 50
 GAG_HV1Y2
 ID GAG_HV1Y2 STANDARD; PRT; 499 AA.
 AC P35962;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=36377;
 RN [1]
 RP SEQUENCE FROM N.A.
 EX MEDLINE=93021387; PubMed=1404605;
 RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
 RA Shaw G.M.;
 RT "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence

RT for limited defectiveness and complementation.";

RL J. Virol. 66:6587-6600(1992).

CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE

CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL

CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM

CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY

CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.

CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY

CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

CC -1- PTM: The p24 protein is phosphorylated.

CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.

CC -----

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CC -----

DR EMBL; M93258; -; NOT_ANNOTATED_CDS.

DR PIR; A44001; A44001.

DR PDB; IF60; 09-OCT-00.

DR PDB; IMFS; 17-JUN-98.

DR InterPro; IPR000721; Gag_p24.

DR InterPro; IPR008916; Retrov capsid C.

DR InterPro; IPR008919; Retrov capsid_N.

DR InterPro; IPR000071; Retrovir_p17.

DR InterPro; IPR001878; Znf_CCHC.

DR Pfam; PF00540; Gag_p17; 1.

DR Pfam; PF00607; Gag_p24; 1.

DR Pfam; PF00098; zf-CCHC; 2.

DR PRINTS; PR00939; C2HCZNFINGER.

DR PRINTS; PR00234; HIV1MATRIX.

DR SMART; SM00343; Znf_C2HC; 2.

DR PROSITE; PS50158; ZF_CCHC; 2.

KW AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;

KW Zinc-finger; Repeat; 3D-structure; Lipoprotein.

FT INIT MET 0 0

FT CHAIN 1 131

FT CHAIN 132 362

FT CHAIN 363 376

FT CHAIN 377 431

FT CHAIN 432 447

FT CHAIN 448 499

FT CHAIN 499 406

FT ZN_FING 389 406

FT ZN_FING 410 427

FT LIPID 1 1

SQ SEQUENCE 499 AA; 55660 MW; 278E665F5405CD99 CRC64;

Query Match 88.6%; Score 31; DB 1; Length 499;

Best Local Similarity 100.0%; Pred.No.75;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKW 5

Db 11 ELDKW 15

Search completed: March 16, 2004, 09:16:51

Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2004, 09:11:00 ; Search time 39 Seconds
(without alignments)
48.541 Million cell updates/sec

Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDRWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 500 summaries

Database :

SPTREMBL 25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	34	15	Q69904 human immun
2	35	100.0	34	15	Q69905 human immun
3	35	100.0	34	15	Q69893 human immun
4	35	100.0	34	15	Q69903 human immun
5	35	100.0	34	15	Q69894 human immun
6	35	100.0	41	15	Q69891 human immun
7	35	100.0	41	15	Q69892 human immun
8	35	100.0	42	15	Q69910 human immun
9	35	100.0	49	15	Q69896 human immun
10	35	100.0	49	15	Q69906 human immun
11	35	100.0	49	15	Q69907 human immun
12	35	100.0	49	15	Q69895 human immun
13	35	100.0	49	15	Q69909 human immun
14	35	100.0	50	15	Q69898 human immun
15	35	100.0	57	15	Q69913 human immun
16	35	100.0	57	15	Q69912 human immun

Q69911	human immun	Q69911	57	15	35	100.0	17
Q9qgn5	human immun	Q9qgn5	117	15	35	100.0	18
Q9yrs9	human immun	Q9yrs9	117	15	35	100.0	19
Q9yvw7	human immun	Q9yvw7	117	15	35	100.0	20
Q9yrs2	human immun	Q9yrs2	117	15	35	100.0	21
Q9yvw1	human immun	Q9yvw1	117	15	35	100.0	22
Q9esr1	human immun	Q9esr1	118	15	35	100.0	23
Q9es63	human immun	Q9es63	118	15	35	100.0	24
Q9es52	human immun	Q9es52	118	15	35	100.0	25
Q9y202	human immun	Q9y202	118	15	35	100.0	26
Q9ea94	human immun	Q9ea94	122	15	35	100.0	27
Q9yxu9	human immun	Q9yxu9	122	15	35	100.0	28
Q9ea85	human immun	Q9ea85	122	15	35	100.0	29
Q9ea81	human immun	Q9ea81	122	15	35	100.0	30
Q9yxg0	human immun	Q9yxg0	122	15	35	100.0	31
Q9giw4	human immun	Q9giw4	122	15	35	100.0	32
Q9ea44	human immun	Q9ea44	122	15	35	100.0	33
Q9giw0	human immun	Q9giw0	122	15	35	100.0	34
Q9ijn1	human immun	Q9ijn1	122	15	35	100.0	35
Q9wqz0	human immun	Q9wqz0	122	15	35	100.0	36
Q9yxr6	human immun	Q9yxr6	122	15	35	100.0	37
Q9giu3	human immun	Q9giu3	122	15	35	100.0	38
Q9ea55	human immun	Q9ea55	122	15	35	100.0	39
Q9ijn8	human immun	Q9ijn8	122	15	35	100.0	40
Q9ea22	human immun	Q9ea22	122	15	35	100.0	41
Q90px7	human immun	Q90px7	122	15	35	100.0	42
Q9wqz1	human immun	Q9wqz1	122	15	35	100.0	43
Q9ea99	human immun	Q9ea99	122	15	35	100.0	44
Q9yxr8	human immun	Q9yxr8	122	15	35	100.0	45
Q9ijn5	human immun	Q9ijn5	122	15	35	100.0	46
Q9wqy8	human immun	Q9wqy8	122	15	35	100.0	47
Q9ijq0	human immun	Q9ijq0	122	15	35	100.0	48
Q9yxp7	human immun	Q9yxp7	122	15	35	100.0	49
Q9wqz7	human immun	Q9wqz7	122	15	35	100.0	50
Q9ijn9	human immun	Q9ijn9	122	15	35	100.0	51
Q9yxm9	human immun	Q9yxm9	122	15	35	100.0	52
Q9ea90	human immun	Q9ea90	122	15	35	100.0	53
Q9yxu4	human immun	Q9yxu4	122	15	35	100.0	54
Q9giw9	human immun	Q9giw9	122	15	35	100.0	55
Q9giw7	human immun	Q9giw7	122	15	35	100.0	56
Q9ea84	human immun	Q9ea84	122	15	35	100.0	57
Q9ijp8	human immun	Q9ijp8	122	15	35	100.0	58
Q9wqy9	human immun	Q9wqy9	122	15	35	100.0	59
Q9yxr0	human immun	Q9yxr0	122	15	35	100.0	60
Q9ea97	human immun	Q9ea97	122	15	35	100.0	61
Q9yxp1	human immun	Q9yxp1	122	15	35	100.0	62
Q9giw0	human immun	Q9giw0	122	15	35	100.0	63
Q9yxr4	human immun	Q9yxr4	122	15	35	100.0	64
Q9yxq1	human immun	Q9yxq1	122	15	35	100.0	65
Q90px8	human immun	Q90px8	122	15	35	100.0	66
Q9ea93	human immun	Q9ea93	122	15	35	100.0	67
Q9yxq8	human immun	Q9yxq8	122	15	35	100.0	68
Q9yxr1	human immun	Q9yxr1	122	15	35	100.0	69
Q9qiv1	human immun	Q9qiv1	122	15	35	100.0	70
Q9yxr2	human immun	Q9yxr2	122	15	35	100.0	71
Q9qiw2	human immun	Q9qiw2	122	15	35	100.0	72
Q9ea89	human immun	Q9ea89	122	15	35	100.0	73
Q9yxu0	human immun	Q9yxu0	122	15	35	100.0	74
Q9ijq3	human immun	Q9ijq3	122	15	35	100.0	75
Q9qiw5	human immun	Q9qiw5	122	15	35	100.0	76
Q9qiw4	human immun	Q9qiw4	122	15	35	100.0	77
Q9yxr7	human immun	Q9yxr7	122	15	35	100.0	78
Q9ijn6	human immun	Q9ijn6	122	15	35	100.0	79
Q90px0	human immun	Q90px0	122	15	35	100.0	80
Q9ijq6	human immun	Q9ijq6	122	15	35	100.0	81
Q9ijn3	human immun	Q9ijn3	122	15	35	100.0	82
Q9yxp2	human immun	Q9yxp2	122	15	35	100.0	83
Q9ijp2	human immun	Q9ijp2	122	15	35	100.0	84
Q9yxu1	human immun	Q9yxu1	122	15	35	100.0	85
Q9ijq1	human immun	Q9ijq1	122	15	35	100.0	86
Q9ea80	human immun	Q9ea80	122	15	35	100.0	87
Q9ijq9	human immun	Q9ijq9	122	15	35	100.0	88
Q9ijr0	human immun	Q9ijr0	122	15	35	100.0	89

90	35	100.0	122	15	Q9EA92	O9ea92 human immun	163	35	100.0	144	15	Q7ZCC1	Q7zcc1 human immun
91	35	100.0	122	15	Q9YXP4	O9yxp4 human immun	164	35	100.0	144	15	Q7ZCB9	Q7zcb9 human immun
92	35	100.0	122	15	Q9IUQ2	Q9i1q2 human immun	165	35	100.0	144	15	Q7ZCB8	Q7zcb8 human immun
93	35	100.0	122	15	Q9EA82	Q9ea82 human immun	166	35	100.0	144	15	Q7ZCB7	Q7zcb7 human immun
94	35	100.0	122	15	Q9IJP1	Q9i1jp1 human immun	167	35	100.0	144	15	Q7ZCB6	Q7zcb6 human immun
95	35	100.0	122	15	Q90DJ7	Q90dj7 human immun	168	35	100.0	144	15	Q7ZCB5	Q7zcb5 human immun
96	35	100.0	122	15	Q90DL6	Q90dl6 human immun	169	35	100.0	144	15	Q7ZCB4	Q7zcb4 human immun
97	35	100.0	122	15	Q9WR00	Q9wr00 human immun	170	35	100.0	144	15	Q7ZCB3	Q7zcb3 human immun
98	35	100.0	122	15	Q9YXN5	Q9yxns human immun	171	35	100.0	144	15	Q7ZCB2	Q7zcb2 human immun
99	35	100.0	122	15	Q9QIU8	Q9qiu8 human immun	172	35	100.0	144	15	Q7ZCB1	Q7zcb1 human immun
100	35	100.0	122	15	Q9YXP0	Q9yxp0 human immun	173	35	100.0	144	15	Q7ZCB0	Q7zcb0 human immun
101	35	100.0	122	15	Q9YXQ2	Q9yxq2 human immun	174	35	100.0	144	15	Q7ZCA9	Q7zca9 human immun
102	35	100.0	122	15	Q9IJP7	Q9i1jp7 human immun	175	35	100.0	144	15	Q7ZCA8	Q7zca8 human immun
103	35	100.0	122	15	Q9IJP3	Q9i1jp3 human immun	176	35	100.0	144	15	Q7ZCA3	Q7zca3 human immun
104	35	100.0	122	15	Q7ZJUS0	Q7zjso human immun	177	35	100.0	144	15	Q7ZCA2	Q7zca2 human immun
105	35	100.0	122	15	Q7ZJUS9	Q7zjso human immun	178	35	100.0	144	15	Q7ZCA1	Q7zca1 human immun
106	35	100.0	122	15	Q7ZJR8	Q7zjr8 human immun	179	35	100.0	144	15	Q7ZCA0	Q7zca0 human immun
107	35	100.0	122	15	Q7ZJR7	Q7zjr7 human immun	180	35	100.0	144	15	Q7ZC99	Q7zc99 human immun
108	35	100.0	122	15	Q7ZJR6	Q7zjr6 human immun	181	35	100.0	144	15	Q7ZC96	Q7zc96 human immun
109	35	100.0	122	15	Q7ZJR5	Q7zjr5 human immun	182	35	100.0	144	15	Q7ZC95	Q7zc95 human immun
110	35	100.0	122	15	Q7ZJR4	Q7zjr4 human immun	183	35	100.0	144	15	Q7ZC94	Q7zc94 human immun
111	35	100.0	122	15	Q7ZJQ3	Q7zjq3 human immun	184	35	100.0	144	15	Q7ZC93	Q7zc93 human immun
112	35	100.0	122	15	Q7ZJQ2	Q7zjq2 human immun	185	35	100.0	144	15	Q7ZC91	Q7zc91 human immun
113	35	100.0	122	15	Q7ZJQ1	Q7zjq1 human immun	186	35	100.0	144	15	Q7ZC88	Q7zc88 human immun
114	35	100.0	122	15	Q7ZJQ0	Q7zjq0 human immun	187	35	100.0	144	15	Q7ZC87	Q7zc87 human immun
115	35	100.0	122	15	Q7ZJP9	Q7zjp9 human immun	188	35	100.0	144	15	Q7ZC86	Q7zc86 human immun
116	35	100.0	122	15	Q7ZJP8	Q7zjp8 human immun	189	35	100.0	144	15	Q7ZC85	Q7zc85 human immun
117	35	100.0	122	15	Q7ZJP7	Q7zjp7 human immun	190	35	100.0	144	15	Q7ZC84	Q7zc84 human immun
118	35	100.0	122	15	Q7ZJP6	Q7zjp6 human immun	191	35	100.0	144	15	Q7ZC83	Q7zc83 human immun
119	35	100.0	122	15	Q8J3S3	Q8j3s3 human immun	192	35	100.0	144	15	Q7ZC74	Q7zc74 human immun
120	35	100.0	123	15	Q8UM65	Q8umes human immun	193	35	100.0	144	15	Q7ZC73	Q7zc73 human immun
121	35	100.0	123	15	Q9EAA3	Q9eaa3 human immun	194	35	100.0	144	15	Q7ZC71	Q7zc71 human immun
122	35	100.0	123	15	Q9YXR3	Q9yxr3 human immun	195	35	100.0	144	15	Q7ZC70	Q7zc70 human immun
123	35	100.0	123	15	Q8AEX5	Q8aex5 human immun	196	35	100.0	144	15	Q7ZC45	Q7zc45 human immun
124	35	100.0	123	15	Q8AEX4	Q8aex4 human immun	197	35	100.0	145	15	Q7ZC57	Q7zc57 human immun
125	35	100.0	123	15	Q8AEX2	Q8aex2 human immun	198	35	100.0	145	15	Q7ZC56	Q7zc56 human immun
126	35	100.0	123	15	Q8AEX1	Q8aex1 human immun	199	35	100.0	145	15	Q7ZC55	Q7zc55 human immun
127	35	100.0	124	15	Q8J3R7	Q8j3r7 human immun	200	35	100.0	145	15	Q7ZC54	Q7zc54 human immun
128	35	100.0	127	11	Q9D4Q2	Q9d4q2 mus musculus	201	35	100.0	146	15	Q7SM37	Q7sm37 human immun
129	35	100.0	127	15	Q9YXQ0	Q9yxx0 human immun	202	35	100.0	147	15	Q7SLY9	Q7sly9 human immun
130	35	100.0	127	15	Q9YZ16	Q9yz16 human immun	203	35	100.0	153	15	Q8JM03	Q8jm03 human immun
131	35	100.0	129	15	Q9YV25	Q9yv25 human immun	204	35	100.0	155	15	Q8J3P4	Q8j3p4 human immun
132	35	100.0	130	15	Q90Q14	Q90q14 human immun	205	35	100.0	155	15	Q8J3P8	Q8j3p8 human immun
133	35	100.0	132	15	Q90Q52	Q90q52 human immun	206	35	100.0	155	15	Q8J3P6	Q8j3p6 human immun
134	35	100.0	132	15	Q90Q02	Q90q02 human immun	207	35	100.0	155	15	Q8J3N5	Q8j3n5 human immun
135	35	100.0	132	15	Q91WQ5	Q91wq5 human immun	208	35	100.0	155	15	Q8J3N2	Q8j3n2 human immun
136	35	100.0	132	15	Q7SLZ2	Q7slz2 human immun	209	35	100.0	155	15	Q8J3N1	Q8j3n1 human immun
137	35	100.0	133	15	Q90Q30	Q90q30 human immun	210	35	100.0	155	15	Q8J3N0	Q8j3n0 human immun
138	35	100.0	133	15	Q90Q57	Q90q57 human immun	211	35	100.0	159	15	Q8JER6	Q8jer6 human immun
139	35	100.0	133	15	Q90Q63	Q90q63 human immun	212	35	100.0	161	15	Q8JER1	Q8jer1 human immun
140	35	100.0	133	15	Q90Q53	Q90q53 human immun	213	35	100.0	163	15	Q90E80	Q90e80 human immun
141	35	100.0	133	15	Q90Q20	Q90q20 human immun	214	35	100.0	163	15	Q90E69	Q90e69 human immun
142	35	100.0	138	15	Q7SLZ3	Q7slz3 human immun	215	35	100.0	163	15	Q90E77	Q90e77 human immun
143	35	100.0	139	15	Q7SLZ9	Q7slz9 human immun	216	35	100.0	163	15	Q90E68	Q90e68 human immun
144	35	100.0	142	15	Q7ZCF7	Q7zcf7 human immun	217	35	100.0	163	15	Q90E63	Q90e63 human immun
145	35	100.0	143	15	Q7ZC46	Q7zcf6 human immun	218	35	100.0	163	15	Q90E79	Q90e79 human immun
146	35	100.0	143	15	Q7SM06	Q7sm06 human immun	219	35	100.0	163	15	Q90E61	Q90e61 human immun
147	35	100.0	144	15	Q7ZCF1	Q7zcf1 human immun	220	35	100.0	163	15	Q90E71	Q90e71 human immun
148	35	100.0	144	15	Q7ZCF0	Q7zcf0 human immun	221	35	100.0	163	15	Q90E74	Q90e74 human immun
149	35	100.0	144	15	Q7ZC88	Q7zcf8 human immun	222	35	100.0	163	15	Q90E75	Q90e75 human immun
150	35	100.0	144	15	Q7ZC84	Q7zcf4 human immun	223	35	100.0	163	15	Q90E72	Q90e72 human immun
151	35	100.0	144	15	Q7ZC83	Q7zcf3 human immun	224	35	100.0	163	15	Q90E60	Q90e60 human immun
152	35	100.0	144	15	Q7ZC82	Q7zcf2 human immun	225	35	100.0	163	15	Q90E56	Q90e56 human immun
153	35	100.0	144	15	Q7ZC81	Q7zcf1 human immun	226	35	100.0	163	15	Q90E66	Q90e66 human immun
154	35	100.0	144	15	Q7ZC80	Q7zcf8 human immun	227	35	100.0	163	15	Q90E78	Q90e78 human immun
155	35	100.0	144	15	Q7ZC87	Q7zcd7 human immun	228	35	100.0	164	15	Q90E81	Q90e81 human immun
156	35	100.0	144	15	Q7ZC86	Q7zcd6 human immun	229	35	100.0	164	15	Q8JER5	Q8jer5 human immun
157	35	100.0	144	15	Q7ZC83	Q7zcd3 human immun	230	35	100.0	164	15	Q90E64	Q90e64 human immun
158	35	100.0	144	15	Q7ZC82	Q7zcd2 human immun	231	35	100.0	164	15	Q90E70	Q90e70 human immun
159	35	100.0	144	15	Q7ZC81	Q7zcd1 human immun	232	35	100.0	164	15	Q90E82	Q90e82 human immun
160	35	100.0	144	15	Q7ZC80	Q7zcd0 human immun	233	35	100.0	164	15	Q8JER2	Q8jer2 human immun
161	35	100.0	144	15	Q7ZC89	Q7zcc9 human immun	234	35	100.0	167	15	Q8JAM3	Q8jam3 human immun
162	35	100.0	144	15	Q7ZCC2	Q7zcc2 human immun	235	35	100.0	168	15		

236	35	100.0	169	15	O8JER0	O8jer0 human immun
237	35	100.0	169	15	O8JER9	O8jed9 human immun
238	35	100.0	173	15	O8JAU9	O8jaj9 human immun
239	35	100.0	178	15	O8JAM4	O8jam4 human immun
240	35	100.0	179	15	O8JAK7	O8jak7 human immun
241	35	100.0	190	15	O8JAJ7	O8jai7 human immun
242	35	100.0	192	15	O8JAL2	O8jal2 human immun
243	35	100.0	195	15	O8JAY4	O8jay4 human immun
244	35	100.0	199	15	O8JAL3	O8jal3 human immun
245	35	100.0	199	15	O8JAL6	O8jal6 human immun
246	35	100.0	201	15	O8JAL5	O8jal5 human immun
247	35	100.0	201	15	O8JAL8	O8jal8 human immun
248	35	100.0	202	15	O8JAK5	O8jak5 human immun
249	35	100.0	218	15	O8JAM1	O8jam1 human immun
250	35	100.0	219	15	O8JAU4	O8jaj4 human immun
251	35	100.0	245	15	O8JF92	O8jfs2 human immun
252	35	100.0	266	11	O9CPY3	O9cyp3 mus musculus
253	35	100.0	307	4	O9BVM3	O9bvw3 homo sapien
254	35	100.0	323	11	O8ROF7	O8rof7 mus musculus
255	35	100.0	357	15	O78118	O78118 human immun
256	35	100.0	357	15	O78119	O78119 human immun
257	35	100.0	357	15	O78112	O78112 human immun
258	35	100.0	358	15	O78120	O78120 human immun
259	35	100.0	443	15	O80023	O80023 human immun
260	35	100.0	445	15	O80021	O80021 human immun
261	35	100.0	465	11	O9CXF0	O9cxf0 mus musculus
262	35	100.0	616	15	O993B0	O993b0 human immun
263	35	100.0	618	15	O993B2	O993b2 human immun
264	35	100.0	635	15	O90U82	O90u82 human immun
265	35	100.0	645	15	O993A6	O993a6 human immun
266	35	100.0	668	15	O91JZ3	O91jz3 human immun
267	35	100.0	679	15	O9JUG5	O9jug5 human immun
268	35	100.0	684	15	O9IKO6	O9ik06 human immun
269	35	100.0	698	10	O9IXV2	O9xhv2 oryza sativ
270	35	100.0	724	15	O9QKH4	O9qkh4 human immun
271	35	100.0	727	15	O9Q723	O9q723 human immun
272	35	100.0	727	15	O9QKJ3	O9qkj3 human immun
273	35	100.0	732	15	O9QKJ2	O9qkj2 human immun
274	35	100.0	747	15	O70607	O70607 human immun
275	35	100.0	748	15	O70606	O70606 human immun
276	35	100.0	748	15	O8J582	O8j582 human immun
277	35	100.0	748	15	O8J583	O8j583 human immun
278	35	100.0	749	15	O8J581	O8j581 human immun
279	35	100.0	752	15	O70604	O70604 human immun
280	35	100.0	752	15	O70605	O70605 human immun
281	35	100.0	752	15	O70608	O70608 human immun
282	35	100.0	755	15	O99BW9	O99bw9 human immun
283	35	100.0	756	16	O926P8	O926p8 listeria in
284	35	100.0	757	15	O9Q722	O9q722 human immun
285	35	100.0	766	15	O90VG2	O90vg2 human immun
286	35	100.0	781	15	O70159	O70159 human immun
287	35	100.0	783	15	O99BX4	O99bx4 human immun
288	35	100.0	785	15	O99BX2	O99bx2 human immun
289	35	100.0	788	15	O99BY6	O99by6 human immun
290	35	100.0	789	15	O9QKJ4	O9qkj4 human immun
291	35	100.0	790	15	O99BW8	O99bw8 human immun
292	35	100.0	790	15	O99BY4	O99by4 human immun
293	35	100.0	791	15	O99BX1	O99bx1 human immun
294	35	100.0	793	15	O99BX8	O99bx8 human immun
295	35	100.0	795	15	O99BX6	O99bx6 human immun
296	35	100.0	797	15	O91W14	O91w14 human immun
297	35	100.0	797	15	O99BY2	O99by2 human immun
298	35	100.0	799	15	O99BX5	O99bx5 human immun
299	35	100.0	800	15	O99BY1	O99by1 human immun
300	35	100.0	801	15	O99BY7	O99by7 human immun
301	35	100.0	801	15	O99BY0	O99by0 human immun
302	35	100.0	801	15	O99BX0	O99bx0 human immun
303	35	100.0	801	15	O99BX7	O99bx7 human immun
304	35	100.0	805	15	O99BY5	O99by5 human immun
305	35	100.0	807	15	O99BY2	O99by2 human immun
306	35	100.0	829	15	O76122	O76122 human immun
307	35	100.0	829	15	O78UQ4	O78uq4 human immun
308	35	100.0	829	15	O78UQ3	O78uq3 human immun

309	35	100.0	830	15	O78UQ2	O78uq2 human immun
310	35	100.0	833	15	O9QK14	O9qk14 human immun
311	35	100.0	833	15	O9QKH9	O9qkh9 human immun
312	35	100.0	833	15	O9QK13	O9qk13 human immun
313	35	100.0	835	15	O90VF1	O90vf1 human immun
314	35	100.0	835	15	O76074	O76074 human immun
315	35	100.0	837	15	O9QKJ6	O9qkj6 human immun
316	35	100.0	837	15	O9QKJ5	O9qkj5 human immun
317	35	100.0	838	15	OQ3806	OQ3806 human immun
318	35	100.0	839	15	O73364	O73364 human immun
319	35	100.0	840	15	O70694	O70694 human immun
320	35	100.0	841	15	O9E1S4	O9e1s4 human immun
321	35	100.0	841	15	O9QKJ1	O9qkj1 human immun
322	35	100.0	841	15	O41556	O41556 human immun
323	35	100.0	842	15	O8JBJ5	O8jbj5 human immun
324	35	100.0	843	15	O41610	O41610 human immun
325	35	100.0	843	15	O70150	O70150 human immun
326	35	100.0	843	15	O9QKH8	O9qkh8 human immun
327	35	100.0	843	15	O70008	O70008 human immun
328	35	100.0	844	15	O56561	O56561 human immun
329	35	100.0	845	15	O8UNF5	O8unf5 human immun
330	35	100.0	845	15	O70679	O70679 human immun
331	35	100.0	845	15	O9QR81	O9qrb1 human immun
332	35	100.0	845	15	O78V04	O78v04 human immun
333	35	100.0	845	15	O78PQ3	O78pq3 human immun
334	35	100.0	846	15	O8UL63	O8ul63 human immun
335	35	100.0	846	15	O56111	O56111 human immun
336	35	100.0	846	15	O9PXW7	O9pxw7 human immun
337	35	100.0	847	15	O41537	O41537 human immun
338	35	100.0	847	15	O90DU1	O90du1 human immun
339	35	100.0	847	15	O69996	O69996 human immun
340	35	100.0	847	15	O75760	O75760 human immun
341	35	100.0	847	15	O76125	O76125 human immun
342	35	100.0	847	15	O8Q366	O8q366 human immun
343	35	100.0	847	15	O8A821	O8a821 human immun
344	35	100.0	847	15	O72820	O72b20 human immun
345	35	100.0	848	15	O74999	O74999 human immun
346	35	100.0	848	15	O69988	O69988 human immun
347	35	100.0	848	15	O9E1S3	O9e1s3 human immun
348	35	100.0	848	15	O76123	O76123 human immun
349	35	100.0	848	15	O69990	O69990 human immun
350	35	100.0	848	15	O72821	O72b21 human immun
351	35	100.0	849	15	O74849	O74849 human immun
352	35	100.0	849	15	O9PXE5	O9pxe5 human immun
353	35	100.0	849	15	O77368	O77368 human immun
354	35	100.0	849	15	O9PX00	O9pxx0 human immun
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356	35	100.0	849	15	O91BN3	O91bn3 human immun
357	35	100.0	849	15	O8Q851	O8q851 human immun
358	35	100.0	849	15	O9YUY1	O9yuy1 human immun
359	35	100.0	849	15	O72J31	O72j31 human immun
360	35	100.0	849	15	O72C14	O72c14 human immun
361	35	100.0	849	15	O72C12	O72c12 human immun
362	35	100.0	849	15	O72C10	O72c10 human immun
363	35	100.0	849	15	O78V13	O78v13 human immun
364	35	100.0	849	15	O78KG4	O78kg4 human immun
365	35	100.0	850	15	O41591	O41591 human immun
366	35	100.0	850	15	O8UL57	O8ul57 human immun
367	35	100.0	850	15	O70003	O70003 human immun
368	35	100.0	850	15	O11946	O11946 human immun
369	35	100.0	850	15	O79795	O79795 human immun
370	35	100.0	850	15	O8Q2F2	O8q2f2 human immun
371	35	100.0	850	15	O9WLG7	O9wlg7 human immun
372	35	100.0	850	15	O8UL56	O8ul56 human immun
373	35	100.0	850	15	O8UL58	O8ul58 human immun
374	35	100.0	850	15	O78V14	O78v14 human immun
375	35	100.0	851	15	O994B6	O994b6 human immun
376	35	100.0	851	15	O56110	O56110 human immun
377	35	100.0	851	15	O8Q852	O8q852 human immun
378	35	100.0	851	15	O73361	O73361 human immun
379	35	100.0	851	15	O78243	O78243 human immun
380	35	100.0	851	15	O9E1R6	O9e1r6 human immun
381	35	100.0	851	15	O56562	O56562 human immun

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405 35 100.0 853 15 Q9E1S9 human immun
406 35 100.0 853 15 Q56108 human immun
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410 35 100.0 853 15 Q8UPN0 human immun
411 35 100.0 853 15 Q55774 human immun
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413 35 100.0 853 15 Q9YUY6 human immun
414 35 100.0 853 15 Q56563 human immun
415 35 100.0 853 15 Q8AF21 human immun
416 35 100.0 853 15 Q8AE50 human immun
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418 35 100.0 853 15 Q7SVL6 human immun
419 35 100.0 853 15 Q7SUR3 human immun
420 35 100.0 853 15 Q7SUR2 human immun
421 35 100.0 853 15 Q7S1K0 human immun
422 35 100.0 854 15 Q56566 human immun
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426 35 100.0 854 15 Q91JZ7 human immun
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435 35 100.0 854 15 Q8UPM1 human immun
436 35 100.0 854 15 Q9E1S8 human immun
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441 35 100.0 854 15 Q7SVL3 human immun
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454 35 100.0 855 15 Q8UL62 human immun
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461 35 100.0 855 15 Q902H5 human immun
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463 35 100.0 855 15 Q03805 human immun
464 35 100.0 855 15 Q8AQV7 human immun
465 35 100.0 855 15 Q7SVL0 human immun
466 35 100.0 855 15 Q7SU07 human immun
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468 35 100.0 855 15 Q7SU05 human immun
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470 35 100.0 855 15 Q7SU03 human immun
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473 35 100.0 855 15 Q7SU00 human immun
474 35 100.0 855 15 Q7SUR9 human immun
475 35 100.0 855 15 Q7SUR8 human immun
476 35 100.0 855 15 Q7SUR7 human immun
477 35 100.0 855 15 Q7SUR6 human immun
478 35 100.0 855 15 Q7SUR5 human immun
479 35 100.0 855 15 Q7SUR4 human immun
480 35 100.0 855 15 Q7SUR1 human immun
481 35 100.0 855 15 Q7SU00 human immun
482 35 100.0 856 15 Q9C006 human immun
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488 35 100.0 856 15 Q9YUY4 human immun
489 35 100.0 856 15 Q9FXZ0 human immun
490 35 100.0 856 15 Q74090 human immun
491 35 100.0 856 15 Q9DSL8 human immun
492 35 100.0 856 15 Q705M7 human immun
493 35 100.0 856 15 Q71014 human immun
494 35 100.0 856 15 Q9E1R8 human immun
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496 35 100.0 856 15 Q70200 human immun
497 35 100.0 856 15 Q73295 human immun
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500 35 100.0 856 15 Q72993 human immun
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ALIGNMENTS

RESULT 1

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Q69904 ID Q69904 PRELIMINARY; PRT; 34 AA.
AC Q69904;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06734; AAA19147.1; -.
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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4184 MW; BB1CAA65F131AD5A CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 2
Q69905 PRELIMINARY; PRT; 34 AA.
AC Q69905;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 3
Q69893 PRELIMINARY; PRT; 34 AA.
AC Q69893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 4
Q69903 PRELIMINARY; PRT; 34 AA.
AC Q69903;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 5
Q69894 PRELIMINARY; PRT; 34 AA.
AC Q69894;

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RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 0C7CAA60A164B89C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 4
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AC Q69903;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 5
Q69894 PRELIMINARY; PRT; 34 AA.
AC Q69894;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06724; AAA19137.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
FT NON_TER 34
SQ SEQUENCE 34 AA; 4182 MW; A37CAA60A164AEF0 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 6
Q69891 ID Q69891 PRELIMINARY; PRT; 41 AA.
AC Q69891;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06721; AAA19134.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 41
FT NON_TER 41
SQ SEQUENCE 41 AA; 5082 MW; 0B9C7E2CDDA403C6 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 41;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 7
Q69892 ID Q69892 PRELIMINARY; PRT; 41 AA.
AC Q69892;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06722; AAA19135.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 41
FT NON_TER 41
SQ SEQUENCE 41 AA; 5081 MW; 0B9C70CC33403CC6 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 41;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 8
Q69910 ID Q69910 PRELIMINARY; PRT; 42 AA.
AC Q69910;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06740; AAA19153.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
```

RT	variants and primary isolates by IAM-41-2F5, an anti-gp41 human monoclonal antibody.";
RL	Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR	EMBL; U06736; AAA19149.1; -
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR000328; Env_GP41.
DR	Pfam; PF00517; GP41; 1.
KW	Transmembrane.
FT	NON_TER 1
FT	NON_TER 49 49
SQ	SEQUENCE 49 AA; 6214 MW; 29C4E5A8C8D63DD8 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 49;	
Best Local Similarity 100.0%; Pred. No. 10;	
Matches 6; Conservative 0; Mismatches 0; Indels 0;	
Qy	1 ELDKWA 6
Db	38 ELDKWA 43
RESULT 11	
Q69907	PRELIMINARY; PRT; 49 AA.
ID	Q69907;
AC	Q69907; 1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Gp41 (fragment).
GN	ENV.
OS	Human immunodeficiency virus 1.
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11676;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=94211861; PubMed=7512731;
RA	Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA	Keller P.M., Shaw A.R., Emini E.A.;
RT	"Neutralization of divergent human immunodeficiency virus type 1
RT	variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT	monoclonal antibody.";
RL	Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR	EMBL; U06737; AAA19150.1; -
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR000328; Env_GP41.
DR	Pfam; PF00517; GP41; 1.
KW	Transmembrane.
FT	NON_TER 1
FT	NON_TER 49 49
SQ	SEQUENCE 49 AA; 6241 MW; 29C4E5A8C8C7CDD8 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 49;	
Best Local Similarity 100.0%; Pred. No. 10;	
Matches 6; Conservative 0; Mismatches 0; Indels 0;	
Qy	1 ELDKWA 6
Db	38 ELDKWA 43
RESULT 12	
Q69895	PRELIMINARY; PRT; 49 AA.
ID	Q69895;
AC	Q69895; 1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Gp41 (fragment).
GN	ENV.

```
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06725; AAA19138.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6168 MW; 8077C4815B83281E CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 38 ELDKWA 43

RESULT 13
ID Q69909 PRELIMINARY; PRT; 49 AA.
AC Q69909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06739; AAA19152.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6196 MW; E9B618825B832D1E CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 38 ELDKWA 43

RESULT 14
ID Q69898 PRELIMINARY; PRT; 50 AA.
AC Q69898;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06728; AAA19141.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 50 50
SQ SEQUENCE 50 AA; 6358 MW; EABA093A1C6C79E1 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 39 ELDKWA 44

RESULT 15
ID Q69913 PRELIMINARY; PRT; 57 AA.
AC Q69913;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06743; AAA19156.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 7195 MW; D9AC849ED459FD04 CRC64;
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Query Match      100.0%; Score 35; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      46 ELDKWA 51
|||||

RESULT 16
Q69912      PRELIMINARY;      PRT;      57 AA.
AC Q69912;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06742; AAA19154.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 7123 MW; D9AC849C76D3D704 CRC64;

Query Match      100.0%; Score 35; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      46 ELDKWA 51
|||||

RESULT 17
Q69911      PRELIMINARY;      PRT;      57 AA.
AC Q69911;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06741; AAA19154.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 57
SQ SEQUENCE 57 AA; 7267 MW; C2BC6A9034525CAE CRC64;

Query Match      100.0%; Score 35; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      46 ELDKWA 51
|||||

RESULT 18
Q9QQN5      PRELIMINARY;      PRT;      117 AA.
AC Q9QQN5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=96VSHIPS7;
RA Ellenberger D., Sullivan P.S., Dorn J., Schable C., Spira T.J.,
RA Folks T.M., Lal R.B.;
RT "Viral and Immunologic Examination of HIV-1-infected Persistently
RT Seronegative (HIPS) Persons."
RL Infect. Dis. 0:0-0(1999).
DR EMBL; AF157468; AAD45888.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14011 MW; 9A71687C21470B60 CRC64;

Query Match      100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      102 ELDKWA 107
|||||

RESULT 19
Q9YRS9      PRELIMINARY;      PRT;      117 AA.
AC Q9YRS9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=96USSN94;

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RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RL reveals multiple subtypes of HIV-1 Group M and Group O.";
DR EMBL; AF096337; AAD04412.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13953 MW; FIA8174D1A50B77B CRC64;

Query Match 100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 20
Q9YYW7 Q9YYW7 PRELIMINARY; PRT; 117 AA.
AC Q9YYW7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=326.661;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006939; AAD01383.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13911 MW; CD3E75531269F9C7 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 106 ELDKWA 111

RESULT 21
Q9YRS2 Q9YRS2 PRELIMINARY; PRT; 117 AA.
AC Q9YRS2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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```
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USTG17;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RL reveals multiple subtypes of HIV-1 Group M and Group O.";
DR EMBL; AF096344; AAD04419.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 14004 MW; 11CA37F5C8C6278F CRC64;

Query Match 100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 22
Q9YYW1 Q9YYW1 PRELIMINARY; PRT; 117 AA.
AC Q9YYW1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=503.083;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006951; AAD01395.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 14043 MW; 76573E01C889F22C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 106 ELDKWA 111
```

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RESULT 23
Q9ESR1
ID Q9ESR1 PRELIMINARY; PRT; 118 AA.
AC Q9ESR1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM188;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM188;
RA Fonjungo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngngasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252110; AAG14319.1; -.
DR GO; GO:0016031; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane. 1
KW Transmembrane. 1
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 14377 MW; D972C44345FA07D3 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 98 ELDKWA 103

RESULT 24
Q9ESS3
ID Q9ESS3 PRELIMINARY; PRT; 118 AA.
AC Q9ESS3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM11;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM11;

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RA Fonjungo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngngasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252098; AAG14307.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane. 1
KW Transmembrane. 1
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 14275 MW; 1878D17C292899C0 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 98 ELDKWA 103

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RESULT 25
Q9ESS2
ID Q9ESS2 PRELIMINARY; PRT; 118 AA.
AC Q9ESS2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM110;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM110;
RA Fonjungo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngngasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252099; AAG14308.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane. 1
KW Transmembrane. 1
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 14288 MW; 051B1921BA69276A CRC64;

Query Match 100.0%; Score 35; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 98 ELDKWA 103

RESULT 26

```

Q9YZ02 Q9YZ02 PRELIMINARY; PRT; 118 AA.
AC Q9YZ02;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=151.940;
RA Brennan C.A., Lund J.K., Golden A., Yanaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
RT Uganda."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF006870; AA001314.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 14076 MW; 6FB855B3B1F6C23F CRC64;
Query Match 100.0%; Score 35; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 107 ELDKWA 112
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 107 ELDKWA 112

Q9EA94 Q9EA94 PRELIMINARY; PRT; 122 AA.
AC Q9EA94;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX513;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States."
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190958; AAG02320.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14674 MW; AFDA95E7701E7E5B CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;

Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 102 ELDKWA 107

RESULT 28
Q9YXN9 Q9YXN9 PRELIMINARY; PRT; 122 AA.
AC Q9YXN9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RU96RP089;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034064; AAC79316.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14636 MW; C42C7A900C8C1DB8 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 102 ELDKWA 107

RESULT 29
Q9EA85 Q9EA85 PRELIMINARY; PRT; 122 AA.
AC Q9EA85;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX84;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States."
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190967; AAG02329.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.

```
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14692 MW; F777D665CE19C4E0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 122;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 30
Q9EA81 PRELIMINARY; PRT; 122 AA.
AC Q9EA81;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX923;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States."
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL; AF190971; AAG02333.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14753 MW; C3FE4DB1F8B5BCBD CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 122;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 31
Q9YXQ0 PRELIMINARY; PRT; 122 AA.
AC Q9YXQ0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14692 MW; F777D665CE19C4E0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 122;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 32
Q9QIW4 PRELIMINARY; PRT; 122 AA.
AC Q9QIW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ07;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165540; AAF08485.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14742 MW; B42975291BA5F682 CRC64;

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 122;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 33
Q9EAA4 PRELIMINARY; PRT; 122 AA.
AC Q9EAA4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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Db 102 ELDKWA 107
|||||

RESULT 35
Q91JN1 PRELIMINARY; PRT; 122 AA.

ID Q91JN1
AC Q91JN1; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR52;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosi W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RL heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220701; AAF76820.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14917 MW; 69477A001A80725D CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 ELDKWA 6
|||||

Db 102 ELDKWA 107

RESULT 36
Q9WQZ0 PRELIMINARY; PRT; 122 AA.

ID Q9WQZ0
AC Q9WQZ0;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TH38;
RX Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RL isolates provides an alternate region for subtype determination.";
RL Submitted (DDBJ-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113592; AAD42760.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
FT NON_TER 1
FT NON_TER 122

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SQ SEQUENCE 122 AA; 14860 MW; 9F379DA806F98CED CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 102 ELDKWA 107

RESULT 37
Q9YXR6 PRELIMINARY; PRT; 122 AA.
ID Q9YXR6
AC Q9YXR6
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP004;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A., D.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.,
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034037; AAC79289.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
DR NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14702 MW; 873C9A28AE14BA78 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 102 ELDKWA 107

RESULT 38
Q9QIU3 PRELIMINARY; PRT; 122 AA.
ID Q9QIU3
AC Q9QIU3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERRJ28;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazans A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165561; AAF08506.1; -.

SQ SEQUENCE 122 AA; 14860 MW; 9F379DA806F98CED CRC64;
Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 102 ELDKWA 107

RESULT 39
Q9EAA5 PRELIMINARY; PRT; 122 AA.
ID Q9EAA5
AC Q9EAA5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX126;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL Infect. Dis. 181:470-475(2000).
DR EMBL; AF190947; AAG02309.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Transmembrane.
DR NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14859 MW; E6D2DAD15E71607A CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 102 ELDKWA 107

RESULT 40
Q9IJM8 PRELIMINARY; PRT; 122 AA.
ID Q9IJM8
AC Q9IJM8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=AR58;
RX  MEDLINE=20346416; PubMed=10890362;
RA  Masciotra S., Livellara B., Bellosio W., Clara L., Tanuri A., Ramos A.,
RA  Baggs J., Lal R., Pieniazek D.;
RT  "Evidence for a high frequency of HIV-1 subtype F infections among
RL  heterosexual population in Buenos Aires, Argentina.";
RL  AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR  EMBL; AF220704; AAF76823.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0019031; C:viral envelope; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  InterPro; IPR000328; Env_GP41.
DR  Pfam; PF00517; GP41; 1.
KW  Transmembrane.
FT  NON_TER 1
FT  NON_TER 122
SQ  SEQUENCE 122 AA; 14735 MW; 040891ADC152BEE4 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 ELDKWA 6
Db  102 ELDKWA 107

RESULT 41
Q9EAA2 PRELIMINARY; PRT; 122 AA.
ID Q9EAA2
AC Q9EAA2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RT J. Infect. Dis. 181:470-475 (2000).
DR EMBL; AF190950; AAG02312.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14751 MW; 302E5D7E45ED007D CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 ELDKWA 6
Db  102 ELDKWA 107
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ID Q90PX7 PRELIMINARY; PRT; 122 AA.
AC Q90PX7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21270244; PubMed=11376043;
RA Agwale S.M., Robbins K.E., Odama L., Saekhou A., Zeh C., Eubio A.,
RA Njoku O.M., Sani-Gwarzo N., Gboun M.F., Gao F., Reitz M., Hone D.,
RA Folks T.M., Pieniazek D., Wambele C., Kalish M.L.;
RT "Development of an env gp41-based Heteroduplex Mobility Assay for
RT Rapid Human Immunodeficiency Virus Type 1 Subtyping.";
RL J. Clin. Microbiol. 39:2110-2114 (2001).
DR EMBL; AF343909; AAK66176.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14701 MW; 6A9C8669908E66F1E CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 ELDKWA 6
Db  102 ELDKWA 107

RESULT 43
Q9WQZ1 PRELIMINARY; PRT; 122 AA.
ID Q9WQZ1
AC Q9WQZ1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TH27;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113591; AAD42759.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14847 MW; 4E202AEC6B404A06 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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**GO; GO; GO
interP**

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RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113594; AAD42762.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14816 MW; 3F9D3FAD52DC0503 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 48
Q91JQ0 PRELIMINARY; PRT; 122 AA.
ID Q91JQ0
AC Q91JQ0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR8;
RX MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL; AF220682; AAF74234.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14549 MW; 7C9AE589350B76B5 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 49
Q9YXP7 PRELIMINARY; PRT; 122 AA.
ID Q9YXP7
AC Q9YXP7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
```

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OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP065;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034056; AAC79308.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14791 MW; A96F27C55B01E4CD CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

RESULT 50
Q9WQZ7 PRELIMINARY; PRT; 122 AA.
ID Q9WQZ7
AC Q9WQZ7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CN37;
RA Pieniazek D., Yang C., Lal R.L.;
RT "Phylogenetic analysis of gp41 envelope of HIV-1 groups M, N, and O
RT isolates provides an alternate region for subtype determination.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF113585; AAD42753.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14807 MW; 7744F5AF97830718 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 122;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 102 ELDKWA 107

Search completed: March 16, 2004, 09:17:46
Job time : 49 secs
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103	35	100.0	13	4	US-09-315-304B-269	Sequence 269, App	176	35	100.0	15	3	US-08-484-223B-166	Sequence 166, App
104	35	100.0	13	4	US-09-315-304B-270	Sequence 270, App	177	35	100.0	15	3	US-08-484-223B-167	Sequence 167, App
105	35	100.0	13	4	US-09-315-304B-530	Sequence 530, App	178	35	100.0	15	3	US-08-484-223B-168	Sequence 168, App
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107	35	100.0	13	4	US-08-973-952-22	Sequence 22, App1	180	35	100.0	15	3	US-08-919-597-167	Sequence 167, App
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111	35	100.0	13	4	US-08-973-952-26	Sequence 26, App1	184	35	100.0	15	3	US-08-475-668A-168	Sequence 168, App
112	35	100.0	13	4	US-08-470-896-169	Sequence 169, App	185	35	100.0	15	3	US-08-485-551A-166	Sequence 166, App
113	35	100.0	13	4	US-08-470-896-170	Sequence 170, App	186	35	100.0	15	3	US-08-485-551A-167	Sequence 167, App
114	35	100.0	13	4	US-08-470-896-171	Sequence 171, App	187	35	100.0	15	3	US-08-485-551A-168	Sequence 168, App
115	35	100.0	13	4	US-08-470-896-172	Sequence 172, App	188	35	100.0	15	3	US-08-471-913A-166	Sequence 166, App
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117	35	100.0	13	4	US-08-485-546A-169	Sequence 169, App	190	35	100.0	15	3	US-08-471-913A-168	Sequence 168, App
118	35	100.0	13	4	US-08-485-546A-170	Sequence 170, App	191	35	100.0	15	3	US-08-554-616-54	Sequence 54, App1
119	35	100.0	13	4	US-08-485-546A-171	Sequence 171, App	192	35	100.0	15	3	US-08-485-264A-166	Sequence 166, App
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123	35	100.0	13	4	US-09-834-784-267	Sequence 267, App	196	35	100.0	15	3	US-09-082-279B-372	Sequence 372, App
124	35	100.0	13	4	US-09-834-784-268	Sequence 268, App	197	35	100.0	15	3	US-09-082-279B-373	Sequence 373, App
125	35	100.0	13	4	US-09-834-784-269	Sequence 269, App	198	35	100.0	15	3	US-09-082-279B-513	Sequence 513, App
126	35	100.0	13	4	US-09-834-784-270	Sequence 270, App	199	35	100.0	15	3	US-09-082-279B-514	Sequence 514, App
127	35	100.0	13	4	US-09-834-784-530	Sequence 530, App	200	35	100.0	15	3	US-09-082-279B-515	Sequence 515, App
128	35	100.0	13	4	US-09-834-784-531	Sequence 531, App	201	35	100.0	15	3	US-09-082-279B-792	Sequence 792, App
129	35	100.0	13	4	US-09-515-965A-218	Sequence 218, App	202	35	100.0	15	3	US-08-474-349A-166	Sequence 166, App
130	35	100.0	13	4	US-09-515-965A-267	Sequence 267, App	203	35	100.0	15	4	US-08-474-349A-167	Sequence 167, App
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133	35	100.0	13	4	US-09-515-965A-270	Sequence 270, App	206	35	100.0	15	4	US-08-474-349A-430	Sequence 430, App
134	35	100.0	13	4	US-09-515-965A-530	Sequence 530, App	207	35	100.0	15	4	US-08-474-349A-431	Sequence 431, App
135	35	100.0	13	4	US-09-515-965A-531	Sequence 531, App	208	35	100.0	15	4	US-08-474-349A-432	Sequence 432, App
136	35	100.0	13	4	US-09-350-641C-218	Sequence 218, App	209	35	100.0	15	4	US-09-315-304B-216	Sequence 216, App
137	35	100.0	13	4	US-09-350-641C-267	Sequence 267, App	210	35	100.0	15	4	US-09-315-304B-372	Sequence 372, App
138	35	100.0	13	4	US-09-350-641C-268	Sequence 268, App	211	35	100.0	15	4	US-09-315-304B-373	Sequence 373, App
139	35	100.0	13	4	US-09-350-641C-269	Sequence 269, App	212	35	100.0	15	4	US-09-315-304B-374	Sequence 374, App
140	35	100.0	13	4	US-09-350-641C-270	Sequence 270, App	213	35	100.0	15	4	US-09-315-304B-513	Sequence 513, App
141	35	100.0	13	4	US-09-350-641C-530	Sequence 530, App	214	35	100.0	15	4	US-09-315-304B-514	Sequence 514, App
142	35	100.0	13	4	US-09-350-641C-531	Sequence 531, App	215	35	100.0	15	4	US-09-315-304B-515	Sequence 515, App
143	35	100.0	13	4	US-09-350-641C-531	Sequence 531, App1	216	35	100.0	15	4	US-09-315-304B-792	Sequence 792, App
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147	35	100.0	14	3	US-09-082-279B-229	Sequence 229, App	220	35	100.0	15	4	US-08-470-896-166	Sequence 166, App
148	35	100.0	14	4	US-08-474-349A-427	Sequence 427, App	221	35	100.0	15	4	US-08-470-896-167	Sequence 167, App
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155	35	100.0	14	4	US-09-515-965A-1666	Sequence 1666, App	228	35	100.0	15	4	US-09-834-784-373	Sequence 373, App
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157	35	100.0	14	4	US-09-350-641C-229	Sequence 229, App	230	35	100.0	15	4	US-09-834-784-513	Sequence 513, App
158	35	100.0	15	1	US-08-073-028-54	Sequence 54, App1	231	35	100.0	15	4	US-09-834-784-514	Sequence 514, App
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160	35	100.0	15	1	US-08-257-528B-93	Sequence 93, App1	233	35	100.0	15	4	US-09-834-784-792	Sequence 792, App
161	35	100.0	15	1	US-08-460-602A-59	Sequence 59, App1	234	35	100.0	15	4	US-09-515-965A-372	Sequence 372, App
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166	35	100.0	15	1	US-08-465-217A-93	Sequence 93, App1	239	35	100.0	15	4	US-09-515-965A-792	Sequence 792, App
167	35	100.0	15	2	US-08-464-329A-59	Sequence 59, App1	240	35	100.0	15	4	US-09-515-965A-1667	Sequence 1667, App
168	35	100.0	15	2	US-08-464-329A-93	Sequence 93, App1	241	35	100.0	15	4	US-09-350-641C-216	Sequence 216, App
169	35	100.0	15	2	US-08-462-507A-59	Sequence 59, App1	242	35	100.0	15	4	US-09-350-641C-372	Sequence 372, App
170	35	100.0	15	2	US-08-462-507A-93	Sequence 93, App1	243	35	100.0	15	4	US-09-350-641C-373	Sequence 373, App
171	35	100.0	15	2	US-08-467-881A-59	Sequence 59, App1	244	35	100.0	15	4		
172	35	100.0	15	2	US-08-467-881A-93	Sequence 93, App1	245	35	100.0	15	4		
173	35	100.0	15	3	US-08-486-099-166	Sequence 166, App	246	35	100.0	15	4		

247	35	100.0	15	4	US-09-350-641C-374	Sequence 374, App	320	20	1	US-08-460-602A-55	Sequence 55, Appl
248	35	100.0	15	4	US-09-350-641C-513	Sequence 513, App	321	20	1	US-08-463-966A-55	Sequence 55, Appl
249	35	100.0	15	4	US-09-350-641C-514	Sequence 514, App	322	20	1	US-08-465-217A-55	Sequence 55, Appl
250	35	100.0	15	4	US-09-350-641C-515	Sequence 515, App	323	20	2	US-08-464-329A-55	Sequence 55, Appl
251	35	100.0	15	4	US-09-350-641C-792	Sequence 792, App	324	20	2	US-08-462-507A-55	Sequence 55, Appl
252	35	100.0	16	1	US-08-073-028-55	Sequence 55, Appl	325	20	3	US-08-467-881A-55	Sequence 55, Appl
253	35	100.0	16	3	US-08-554-616-55	Sequence 55, Appl	326	20	3	US-09-071-877-8	Sequence 8, Appl
254	35	100.0	16	3	US-09-082-279B-215	Sequence 215, App	327	20	3	US-09-071-877-12	Sequence 12, Appl
255	35	100.0	16	4	US-08-474-349A-425	Sequence 425, App	328	20	3	US-08-484-223B-238	Sequence 238, App
256	35	100.0	16	4	US-09-315-304B-215	Sequence 215, App	329	20	3	US-08-554-616-59	Sequence 59, Appl
257	35	100.0	16	4	US-09-834-784-215	Sequence 215, App	330	20	3	US-09-082-279B-58	Sequence 58, Appl
258	35	100.0	16	4	US-09-515-965A-215	Sequence 215, App	331	20	3	US-09-082-279B-793	Sequence 793, App
259	35	100.0	16	4	US-09-515-965A-1668	Sequence 1668, App	332	20	3	US-09-045-520-8	Sequence 8, Appl
260	35	100.0	16	4	US-09-350-641C-215	Sequence 215, App	333	20	3	US-09-045-520-12	Sequence 12, Appl
261	35	100.0	17	1	US-08-073-028-56	Sequence 56, Appl	334	20	4	US-08-474-349A-422	Sequence 422, App
262	35	100.0	17	1	US-08-257-528B-61	Sequence 61, Appl	335	20	4	US-09-315-304B-58	Sequence 58, Appl
263	35	100.0	17	1	US-08-460-602A-61	Sequence 61, Appl	336	20	4	US-09-315-304B-793	Sequence 793, App
264	35	100.0	17	1	US-08-463-966A-61	Sequence 61, Appl	337	20	4	US-09-834-784-58	Sequence 58, Appl
265	35	100.0	17	1	US-08-465-217A-61	Sequence 61, Appl	338	20	4	US-09-834-784-793	Sequence 793, App
266	35	100.0	17	1	US-08-464-329A-61	Sequence 61, Appl	339	20	4	US-09-515-965A-58	Sequence 58, Appl
267	35	100.0	17	2	US-08-462-507A-61	Sequence 61, Appl	340	20	4	US-09-515-965A-793	Sequence 793, App
268	35	100.0	17	2	US-08-467-881A-61	Sequence 61, Appl	341	20	4	US-09-515-965A-1672	Sequence 1672, App
269	35	100.0	17	3	US-09-071-877-13	Sequence 13, Appl	342	20	4	US-09-350-641C-58	Sequence 58, Appl
270	35	100.0	17	3	US-08-554-616-56	Sequence 56, Appl	343	20	4	US-09-350-641C-793	Sequence 793, App
271	35	100.0	17	3	US-09-082-279B-214	Sequence 214, App	344	21	1	US-08-073-028-60	Sequence 60, Appl
272	35	100.0	17	3	US-09-045-920-13	Sequence 13, Appl	345	21	3	US-09-071-877-9	Sequence 9, Appl
273	35	100.0	17	4	US-08-474-349A-424	Sequence 424, App	346	21	3	US-08-554-616-60	Sequence 60, Appl
274	35	100.0	17	4	US-09-315-304B-214	Sequence 214, App	347	21	3	US-09-082-279B-1082	Sequence 1082, App
275	35	100.0	17	4	US-09-834-784-214	Sequence 214, App	348	21	3	US-09-082-279B-1083	Sequence 1083, App
276	35	100.0	17	4	US-09-515-965A-214	Sequence 214, App	349	21	3	US-09-082-279B-1362	Sequence 1362, App
277	35	100.0	17	4	US-09-515-965A-1669	Sequence 1669, App	350	21	3	US-09-045-520-9	Sequence 9, Appl
278	35	100.0	17	4	US-09-350-641C-214	Sequence 214, App	351	21	3	US-09-315-304B-1082	Sequence 1082, App
279	35	100.0	18	1	US-08-073-028-57	Sequence 57, Appl	352	21	4	US-09-315-304B-1362	Sequence 1362, App
280	35	100.0	18	1	US-08-257-528B-57	Sequence 57, Appl	353	21	4	US-09-315-304B-1363	Sequence 1363, App
281	35	100.0	18	1	US-08-460-602A-57	Sequence 57, Appl	354	21	4	US-09-834-784-1082	Sequence 1082, App
282	35	100.0	18	1	US-08-463-966A-57	Sequence 57, Appl	355	21	4	US-09-834-784-1083	Sequence 1083, App
283	35	100.0	18	1	US-08-465-217A-57	Sequence 57, Appl	356	21	4	US-09-834-784-1362	Sequence 1362, App
284	35	100.0	18	2	US-08-464-329A-57	Sequence 57, Appl	357	21	4	US-09-834-784-1362	Sequence 1362, App
285	35	100.0	18	2	US-08-462-507A-57	Sequence 57, Appl	358	21	4	US-09-515-965A-1082	Sequence 1082, App
286	35	100.0	18	2	US-08-467-881A-57	Sequence 57, Appl	359	21	4	US-09-515-965A-1083	Sequence 1083, App
287	35	100.0	18	3	US-09-071-877-14	Sequence 14, Appl	360	21	4	US-09-515-965A-1362	Sequence 1362, App
288	35	100.0	18	3	US-08-554-616-57	Sequence 57, Appl	361	21	4	US-09-515-965A-1673	Sequence 1673, App
289	35	100.0	18	3	US-09-082-279B-57	Sequence 57, Appl	362	21	4	US-09-350-641C-1083	Sequence 1083, App
290	35	100.0	18	3	US-09-082-279B-98	Sequence 98, Appl	363	21	4	US-09-350-641C-1083	Sequence 1083, App
291	35	100.0	18	3	US-09-082-279B-98	Sequence 98, Appl	364	21	4	US-09-350-641C-1362	Sequence 1362, App
292	35	100.0	18	3	US-09-045-920-14	Sequence 14, Appl	365	22	1	US-08-073-028-61	Sequence 61, Appl
293	35	100.0	18	4	US-08-474-349A-423	Sequence 423, App	366	22	3	US-08-554-616-61	Sequence 61, Appl
294	35	100.0	18	4	US-09-315-304B-3	Sequence 3, Appl	367	22	4	US-09-515-965A-1674	Sequence 1674, App
295	35	100.0	18	4	US-09-315-304B-57	Sequence 57, Appl	368	23	1	US-08-073-028-62	Sequence 62, Appl
296	35	100.0	18	4	US-09-315-304B-98	Sequence 98, Appl	369	23	1	US-08-218-025A-152	Sequence 152, App
297	35	100.0	18	4	US-09-315-304B-1452	Sequence 1452, App	370	23	1	US-08-257-528B-67	Sequence 67, Appl
298	35	100.0	18	4	US-09-834-784-3	Sequence 3, Appl	371	23	1	US-08-460-602A-67	Sequence 67, Appl
299	35	100.0	18	4	US-09-834-784-57	Sequence 57, Appl	372	23	1	US-08-463-966A-67	Sequence 67, Appl
300	35	100.0	18	4	US-09-834-784-98	Sequence 98, Appl	373	23	1	US-08-465-217A-67	Sequence 67, Appl
301	35	100.0	18	4	US-09-515-965A-3	Sequence 3, Appl	374	23	2	US-08-464-329A-67	Sequence 67, Appl
302	35	100.0	18	4	US-09-515-965A-57	Sequence 57, Appl	375	23	2	US-08-462-507A-67	Sequence 67, Appl
303	35	100.0	18	4	US-09-515-965A-98	Sequence 98, Appl	376	23	2	US-08-467-881A-67	Sequence 67, Appl
304	35	100.0	18	4	US-09-515-965A-1452	Sequence 1452, App	377	23	3	US-08-484-223B-237	Sequence 237, App
305	35	100.0	18	4	US-09-515-965A-1670	Sequence 1670, App	378	23	3	US-08-554-616-62	Sequence 62, Appl
306	35	100.0	18	4	US-09-350-641C-3	Sequence 3, Appl	379	23	3	US-09-082-279B-59	Sequence 59, Appl
307	35	100.0	18	4	US-09-350-641C-57	Sequence 57, Appl	380	23	4	US-08-474-349A-421	Sequence 421, App
308	35	100.0	18	4	US-09-350-641C-98	Sequence 98, Appl	381	23	4	US-09-315-304B-59	Sequence 59, Appl
309	35	100.0	18	4	US-09-350-641C-1452	Sequence 1452, App	382	23	4	US-09-834-784-59	Sequence 59, Appl
310	35	100.0	19	1	US-08-073-028-58	Sequence 58, Appl	383	23	4	US-09-515-965A-59	Sequence 59, Appl
311	35	100.0	19	3	US-09-071-877-19	Sequence 19, Appl	384	23	4	US-09-515-965A-1675	Sequence 1675, App
312	35	100.0	19	3	US-08-554-616-58	Sequence 58, Appl	385	23	4	US-09-350-641C-59	Sequence 59, Appl
313	35	100.0	19	3	US-09-045-920-19	Sequence 19, Appl	386	24	1	US-08-073-028-63	Sequence 63, Appl
314	35	100.0	19	4	US-09-515-965A-1671	Sequence 1671, App	387	24	1	US-08-257-528B-65	Sequence 65, Appl
315	35	100.0	20	1	US-08-073-028-59	Sequence 59, Appl	388	24	1	US-08-460-602A-65	Sequence 65, Appl
316	35	100.0	20	1	US-08-218-025A-7	Sequence 7, Appl	389	24	1	US-08-463-966A-65	Sequence 65, Appl
317	35	100.0	20	1	US-08-218-025A-85	Sequence 85, Appl	390	24	1	US-08-465-217A-65	Sequence 65, Appl
318	35	100.0	20	1	US-08-218-025A-86	Sequence 86, Appl	391	24	2	US-08-464-329A-65	Sequence 65, Appl
319	35	100.0	20	1	US-08-257-528B-55	Sequence 55, Appl	392	24	2	US-08-462-507A-65	Sequence 65, Appl

393	35	100.0	24	2	US-08-467-881A-65	Sequence 65, Appl	466	35	100.0	28	4	US-08-470-896-161	Sequence 161, App
394	35	100.0	24	3	US-08-554-616-63	Sequence 63, Appl	467	35	100.0	28	4	US-08-470-896-162	Sequence 162, App
395	35	100.0	24	3	US-09-029-052-6	Sequence 6, Appl	468	35	100.0	28	4	US-08-485-546A-161	Sequence 161, App
396	35	100.0	24	3	US-09-082-279B-789	Sequence 789, App	469	35	100.0	28	4	US-08-485-546A-162	Sequence 162, App
397	35	100.0	24	3	US-09-082-279B-789	Sequence 789, App	470	35	100.0	28	4	US-09-834-784-231	Sequence 231, App
398	35	100.0	24	4	US-09-315-304B-789	Sequence 789, App	471	35	100.0	28	4	US-09-834-784-232	Sequence 232, App
399	35	100.0	24	4	US-09-315-304B-790	Sequence 790, App	472	35	100.0	28	4	US-09-834-784-377	Sequence 377, App
400	35	100.0	24	4	US-09-834-784-789	Sequence 789, App	473	35	100.0	28	4	US-09-834-784-380	Sequence 380, App
401	35	100.0	24	4	US-09-834-784-790	Sequence 790, App	474	35	100.0	28	4	US-09-515-965A-231	Sequence 231, App
402	35	100.0	24	4	US-09-515-965A-789	Sequence 789, App	475	35	100.0	28	4	US-09-515-965A-232	Sequence 232, App
403	35	100.0	24	4	US-09-515-965A-790	Sequence 790, App	476	35	100.0	28	4	US-09-515-965A-377	Sequence 377, App
404	35	100.0	24	4	US-09-515-965A-1676	Sequence 1676, App	477	35	100.0	28	4	US-09-515-965A-380	Sequence 380, App
405	35	100.0	24	4	US-09-350-641C-789	Sequence 789, App	478	35	100.0	28	4	US-09-515-965A-1680	Sequence 1680, App
406	35	100.0	24	4	US-09-350-641C-790	Sequence 790, App	479	35	100.0	28	4	US-09-350-641C-231	Sequence 231, App
407	35	100.0	25	1	US-08-073-028-64	Sequence 64, Appl	480	35	100.0	28	4	US-09-350-641C-232	Sequence 232, App
408	35	100.0	25	3	US-08-554-616-64	Sequence 64, Appl	481	35	100.0	28	4	US-09-350-641C-377	Sequence 377, App
409	35	100.0	25	3	US-09-515-965A-1677	Sequence 1677, App	482	35	100.0	28	4	US-09-350-641C-380	Sequence 380, App
410	35	100.0	26	1	US-08-073-028-65	Sequence 65, Appl	483	35	100.0	29	1	US-08-073-028-68	Sequence 68, Appl
411	35	100.0	26	1	US-08-257-528B-64	Sequence 64, Appl	484	35	100.0	29	3	US-08-554-616-68	Sequence 68, Appl
412	35	100.0	26	1	US-08-460-602A-64	Sequence 64, Appl	485	35	100.0	29	3	US-09-082-279B-635	Sequence 635, App
413	35	100.0	26	1	US-08-463-966A-64	Sequence 64, Appl	486	35	100.0	29	3	US-09-082-279B-637	Sequence 637, App
414	35	100.0	26	1	US-08-485-217A-64	Sequence 64, Appl	487	35	100.0	29	4	US-08-474-349A-419	Sequence 419, App
415	35	100.0	26	2	US-08-464-329A-64	Sequence 64, Appl	488	35	100.0	29	4	US-09-315-304B-635	Sequence 635, App
416	35	100.0	26	2	US-08-462-507A-64	Sequence 64, Appl	489	35	100.0	29	4	US-09-315-304B-637	Sequence 637, App
417	35	100.0	26	2	US-08-467-881A-64	Sequence 64, Appl	490	35	100.0	29	4	US-09-834-784-635	Sequence 635, App
418	35	100.0	26	3	US-08-484-223B-236	Sequence 236, App	491	35	100.0	29	4	US-09-834-784-637	Sequence 637, App
419	35	100.0	26	3	US-08-554-616-65	Sequence 65, Appl	492	35	100.0	29	4	US-09-515-965A-635	Sequence 635, App
420	35	100.0	26	3	US-08-082-279B-60	Sequence 60, Appl	493	35	100.0	29	4	US-09-515-965A-637	Sequence 637, App
421	35	100.0	26	4	US-08-474-349A-420	Sequence 40, App	494	35	100.0	29	4	US-09-515-965A-1681	Sequence 1681, App
422	35	100.0	26	4	US-09-315-304B-60	Sequence 60, Appl	495	35	100.0	29	4	US-09-350-641C-635	Sequence 635, App
430	35	100.0	27	1	US-08-463-966A-63	Sequence 63, Appl	496	35	100.0	29	4	US-09-350-641C-637	Sequence 637, App
431	35	100.0	27	1	US-08-465-217A-63	Sequence 63, Appl	497	35	100.0	30	1	US-08-073-028-16	Sequence 16, Appl
432	35	100.0	27	2	US-08-464-329A-63	Sequence 63, Appl	498	35	100.0	30	1	US-08-073-028-69	Sequence 69, Appl
433	35	100.0	27	2	US-08-462-507A-63	Sequence 63, Appl	499	35	100.0	30	1	US-08-257-528B-58	Sequence 58, Appl
434	35	100.0	27	2	US-08-467-881A-63	Sequence 66, Appl	500	35	100.0	30	1	US-08-257-528B-62	Sequence 62, Appl
435	35	100.0	27	3	US-08-554-616-66	Sequence 1679, App							
436	35	100.0	27	4	US-09-515-965A-1679	Sequence 1679, App							
437	35	100.0	28	1	US-08-073-028-67	Sequence 67, Appl							
438	35	100.0	28	3	US-08-486-039-161	Sequence 161, App							
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440	35	100.0	28	3	US-08-484-223B-161	Sequence 161, App							
441	35	100.0	28	3	US-08-484-223B-162	Sequence 162, App							
442	35	100.0	28	3	US-08-919-597-161	Sequence 161, App							
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448	35	100.0	28	3	US-08-471-913A-161	Sequence 161, App							
449	35	100.0	28	3	US-08-471-913A-162	Sequence 162, App							
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451	35	100.0	28	3	US-08-485-264A-161	Sequence 161, App							
452	35	100.0	28	3	US-08-485-264A-162	Sequence 162, App							
453	35	100.0	28	3	US-09-082-279B-231	Sequence 231, App							
454	35	100.0	28	3	US-09-082-279B-232	Sequence 232, App							
455	35	100.0	28	3	US-09-082-279B-377	Sequence 377, App							
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460	35	100.0	28	4	US-09-315-304B-231	Sequence 231, App							
461	35	100.0	28	4	US-09-315-304B-232	Sequence 232, App							
462	35	100.0	28	4	US-09-315-304B-377	Sequence 377, App							
463	35	100.0	28	4	US-09-315-304B-380	Sequence 380, App							
464	35	100.0	28	4	US-08-973-952-14	Sequence 14, Appl							
465	35	100.0	28	4	US-08-973-952-15	Sequence 15, Appl							

RESULT 1
US-08-257-528B-69
; Sequence 69, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D. Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163

ALIGNMENTS

; INFORMATION FOR SEQ ID NO: 69:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-257-528B-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 2

US-08-361-479-1
; Sequence 1, Application US/08361479
; Patent No. 5693752

; GENERAL INFORMATION:

; APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,

; APPLICANT: GOTTFRIED; MUSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; MAIWAL

; APPLICANT: GEORG; STEINDL, FRANZ

; TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH

; TITLE OF INVENTION: NEUTRALIZE GENTICALLY DIVERGENT HIV-1 ISOLATES.

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/361,479

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/932,787

; FILING DATE: 29-AUG-1992

; APPLICATION NUMBER: A 987/92

; FILING DATE: 14-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 366.015

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-661-8000

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; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: UNKNOWN

; MOLECULE TYPE:

; DESCRIPTION: PEPTIDE

; HYPOTHETICAL: No

; ORIGINAL SOURCE:

; ORGANISM: HIV-1

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE:

; INDIVIDUAL ISOLATE: BH10

; CELL LINE:

; ORGANELLE:

; FEATURE:

; NAME/KEY: GPI60 FRAGMENT

; LOCATION: RESIDUE 662 TO 667

; IDENTIFICATION METHOD:

; OTHER INFORMATION: EPIOTOPE OF HUMAN MONOCLONAL ANTIBODY

; OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160

US-08-361-479-1

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 3

US-08-473-576-1

; Sequence 1, Application US/08473576

; Patent No. 5756674

; GENERAL INFORMATION:

; APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,

; APPLICANT: GOTTFRIED; MUSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; MAIWAL

; APPLICANT: GEORG; STEINDL, FRANZ

; TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH

; TITLE OF INVENTION: NEUTRALIZE GENTICALLY DIVERGENT HIV-1 ISOLATES.

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN

; STREET: 600 THIRD AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/473,576

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/361,479

; FILING DATE: 22-DEC-1994

; APPLICATION NUMBER: 07/932,787

; FILING DATE: 29-AUG-1992

; APPLICATION NUMBER: A 987/92

; FILING DATE: 14-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 366.015

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-661-8000

; TELEFAX: 212-661-8002

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: UNKNOWN

; MOLECULE TYPE:

; DESCRIPTION: PEPTIDE

; HYPOTHETICAL: No

; ORIGINAL SOURCE:

; ORGANISM: HIV-1

; STRAIN:

; INDIVIDUAL ISOLATE: BH10

DEVELOPMENTAL STAGE:

HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:

FEATURE:

NAME/KEY: GPI60 FRAGMENT
LOCATION: RESIDUE 662 TO 667
IDENTIFICATION METHOD:
OTHER INFORMATION: EPIOTOPE OF HUMAN MONOCLONAL ANTIBODY
OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160
US-08-473-576-1

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 4

US-08-460-602A-69
Sequence 69, Application US/08460602A
Patent No. 5759769

GENERAL INFORMATION:

APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/460.602A
APPLICATION NUMBER: 08/460.602A
FILING DATE: 02-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jfb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-460-602A-69

Query Match 100.0%; Score 35; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 5

US-08-323-192D-47
Sequence 47, Application US/08323192D
Patent No. 5786199

GENERAL INFORMATION:

APPLICANT: Palese, Peter
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/323,192D
APPLICATION NUMBER: 08/323,192D
FILING DATE: 14-OCT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-035
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-323-192D-47

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 6

US-08-463-966A-69

Sequence 69, Application US/08463966A
Patent No. 5795955

GENERAL INFORMATION:

APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto

STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463.966A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 7
US-08-465-217A-69
Sequence 69, Application US/08465217A
Patent No. 580822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-217A-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 8
US-08-464-329A-69
Sequence 69, Application US/08464329A
Patent No. 581754
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,329A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids

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;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-329A-69

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 9
US-08-021-879-1
; Sequence 1, Application US/08021879
; Patent No. 5817767
; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway
; APPLICANT: Paul J. Maddon
; TITLE OF INVENTION: SYNERGISTIC COMPOSITION OF CD4-BASED
; TITLE OF INVENTION: PROTEIN AND ANTI-HIV-1 ANTIBODY, AND
; TITLE OF INVENTION: METHODS OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,879
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41189/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOPUI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-021-879-1

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 10
US-08-470-887A-46
; Sequence 46, Application US/08470887A
; Patent No. 5820871
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,887A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-470-887A-46

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 11
US-08-252-508B-46
; Sequence 46, Application US/08252508B
; Patent No. 5854037
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; APPLICANT: Garcia-Sastre, Adolfo
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,508B
; FILING DATE: 01-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
```

; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-252-508B-46

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 12
US-08-975-699-23
; Sequence 23, Application US/08975699
; Patent No. 5858369
; GENERAL INFORMATION:
; APPLICANT: MATSUO, KAZUHIRO
; APPLICANT: CHUJO, YOSHITOMO
; APPLICANT: YAMAZAKI, AKIHIRO
; APPLICANT: HONDA, MITSUO
; APPLICANT: YAMAKAZI, SHUDO
; APPLICANT: TASAKA, HIROMICHI
; TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
; TITLE OF INVENTION: VACCINE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,699
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/619,512
; FILING DATE: 29-MAR-1996
; APPLICATION NUMBER: PCT/JP95/01515
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 178462/1994
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-795-0X PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; STRAIN: HIV-1
; US-08-975-699-23

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 13
US-08-417-210A-147
; Sequence 147, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,210A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; US-08-417-210A-147

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 14
US-08-843-718-1
; Sequence 1, Application US/08843718
; Patent No. 5866694
; GENERAL INFORMATION:

;; APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,
;; APPLICANT: GOTTFRED; MUSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; MAIWAL
;; APPLICANT: GEORG; STEINDL, FRANZ
;; TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH
;; TITLE OF INVENTION: NEUTRALIZE GENTICALLY DIVERGENT HIV-1 ISOLATES.
;; NUMBER OF SEQUENCES: 50
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BIERMAN & MUSERLIAN
;; STREET: 600 THIRD AVENUE
;; CITY: NEW YORK
;; STATE: NEW YORK
;; COUNTRY: USA
;; ZIP: 10016
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/843,718
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/932,787
;; FILING DATE: 29-AUG-1992
;; APPLICATION NUMBER: A 987/92
;; FILING DATE: 14-MAY-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CHARLES A. MUSERLIAN
;; REGISTRATION NUMBER: 19,683
;; REFERENCE/DOCKET NUMBER: 366.015
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-661-8000
;; TELEFAX: 212-661-8002
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6
;; TYPE: AMINO ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: UNKNOWN
;; MOLECULE TYPE:
;; DESCRIPTION: PEPTIDE
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; ORGANISM: HIV-1
;; STRAIN:
;; INDIVIDUAL ISOLATE: BH10
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; FEATURE:
;; NAME/KEY: GP160 FRAGMENT
;; LOCATION: RESIDUE 662 TO 667
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION: EPITOPE OF HUMAN MONOCLONAL ANTIBODY
;; OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160
US-08-843-718-1
Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 1 ELDKWA 6
RESULT 15
US-08-462-507A-69
; Sequence 69, Application US/08462507A

;; Patent No. 5876731
;; GENERAL INFORMATION:
;; APPLICANT: SIA, Charles D.Y.
;; APPLICANT: CHONG, Pele
;; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
;; NUMBER OF SEQUENCES: 101
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: Suite 701, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/462,507A
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/257,528
;; FILING DATE: 09-JUN-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/073,378
;; FILING DATE: 09-JUN-1993
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEWART, MICHAEL I.
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-451 MTS:jb
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 69:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-462-507A-69
Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELDKWA 6
Db 1 ELDKWA 6
RESULT 16
US-08-972-089-23
; Sequence 23, Application US/08972089
; Patent No. 5885580
; GENERAL INFORMATION:
; APPLICANT: MATSUO, KAZUHIRO
; APPLICANT: CHUJO, YOSHITOMO
; APPLICANT: YAMAZAKI, AKIHIRO
; APPLICANT: HONDA, MITSUO
; APPLICANT: YAMAKAZI, SHUDO
; APPLICANT: TASAKA, HIROMICHI
; TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972.089
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975.699
FILING DATE:
FILING DATE: 31-JUL-1995
APPLICATION NUMBER: PCT/JP95/01515
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 178462/1994
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-795-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
STRAIN: HIV-1
US-08-972-089-23

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 17
US-08-467-881A-69
Sequence 69, Application US/08467881A
Patent No. 5951986
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.881A

FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-488 MIS:jdb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-881A-69

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 18
US-09-106-377-46
Sequence 46, Application US/09106377
Patent No. 6001634
GENERAL INFORMATION:
APPLICANT: Palese, Peter
APPLICANT: Garcia-Sastre, Adolfo
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,377
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,508
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:

;
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-106-377-46

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 19

US-09-124-900-11
Sequence 11, Application US/09124900
Patent No. 6268484

GENERAL INFORMATION:

APPLICANT: KATINGER, Hermann
APPLICANT: BUCHACHER, Andrea
APPLICANT: ERNST, Wolfgang
APPLICANT: BALLAUN, Claudia
APPLICANT: PURTSCHER, Martin
APPLICANT: TRKOLA, Alexandra
APPLICANT: FREDL, Renate
APPLICANT: SCHMATZ, Christine
APPLICANT: KLIMA, Annelies
APPLICANT: STEINDL, Franz
APPLICANT: MUSTER, Thomas
TITLE OF INVENTION: HIV-Vaccines

FILE REFERENCE: 1939-112P
CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIORITY APPLICATION NUMBER: PCT/EP95/01481
PRIORITY FILING DATE: 1995-04-19

NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 11

LENGTH: 6

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-124-900-11

Query Match 100.0%; Score 35; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 20

US-09-340-798A-53
Sequence 53, Application US/09340798A
Patent No. 6534312

GENERAL INFORMATION:

APPLICANT: SHIVER, JOHN W.
LIU, MARGARET A.
PERRY, HELEN C.
DAVIES, MARY-ELLEN M.
FREDL, DANIEL C.

TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: US

ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,798A
FILING DATE: 28-Jun-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/877,418
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: HAND, J. MARK

REGISTRATION NUMBER: 36,545

REFERENCE/DOCKET NUMBER: 19729Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3905

TELEFAX: 908-594-4720

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-09-340-798A-53

Query Match 100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 21

US-09-136-159A-147
Sequence 147, Application US/09136159A
Patent No. 6596279

GENERAL INFORMATION:

APPLICANT: Virogenetics Corporation

APPLICANT: Paoletti, Enzo

APPLICANT: Tartaglia, James

APPLICANT: Cox, William I

TITLE OF INVENTION: Immunodeficiency recombinant poxvirus

FILE REFERENCE: 454310-2690.1

CURRENT APPLICATION NUMBER: US/09/136,159A

CURRENT FILING DATE: 1998-08-14

PRIOR APPLICATION NUMBER: US 08/417,210

PRIOR FILING DATE: 1995-04-05

PRIOR APPLICATION NUMBER: US 08/223,842

PRIOR FILING DATE: 1994-04-06

PRIOR APPLICATION NUMBER: US 07/897,382

PRIOR FILING DATE: 1992-06-11

PRIOR APPLICATION NUMBER: US 07/715,921

PRIOR FILING DATE: 1991-06-14

PRIOR APPLICATION NUMBER: US 08/105,483

PRIOR FILING DATE: 1993-08-12

PRIOR APPLICATION NUMBER: US 07/847,951

PRIOR FILING DATE: 1992-03-06

PRIOR APPLICATION NUMBER: US 07/713,967

PRIOR FILING DATE: 1991-06-11

PRIOR APPLICATION NUMBER: US 07/666,056

PRIOR FILING DATE: 1991-03-07

NUMBER OF SEQ ID NOS: 149

SOFTWARE: Patentin version 3.1

SEQ ID NO 147

LENGTH: 6

TYPE: PRT


```
; ORGANISM: Human immunodeficiency virus type 1
US-09-136-159A-147

Query Match          100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 22
US-09-525-874-1
; Sequence 1, Application US/09525874
; Patent No. 6596497
; GENERAL INFORMATION:
; APPLICANT: Jiang, Shibo
; APPLICANT: Debnath, Asim K.
; TITLE OF INVENTION: Screening of Antiviral Compounds
; TITLE OF INVENTION: Targeted to the HIV-1 gp41 Core Structure
; FILE REFERENCE: 990006/RSB
; CURRENT APPLICATION NUMBER: US/09/525,874
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: US 60/124,907
; EARLIER FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Epitope recognized by human MAb 2F5
; FEATURE:
; LOCATION: 662..667
US-09-525-874-1

Query Match          100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 23
US-09-873-459A-4
; Sequence 4, Application US/09873459A
; Patent No. 6627202
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-873-459A-4

Query Match          100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

; ORGANISM: Human immunodeficiency virus type 1
US-09-136-159A-147

Query Match          100.0%; Score 35; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 24
US-08-257-528B-98
; Sequence 98, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIs:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-257-528B-98

Query Match          100.0%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 25
US-08-460-602A-98
; Sequence 98, Application US/08460602A
; Patent No. 5759769
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/460,602A
APPLICATION NUMBER: 24,973
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-602A-98

Query Match 100.0%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 26
US-08-463-966A-98
Sequence 98, Application US/08463966A
Patent No. 5795955
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,966A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-98

Query Match 100.0%; Score 35; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 27
US-08-465-217A-98
Sequence 98, Application US/08465217A
Patent No. 5800822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-217A-98

Query Match 100.0%; Score 35; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0; Mismatches 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 28

US-08-464-329A-98
; Sequence 98, Application US/08464329A
; Patent No. 5817754
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464.329A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-329A-98

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 29

US-08-462-507A-98
; Sequence 98, Application US/08462507A
; Patent No. 5876731
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele

; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,507A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-462-507A-98

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 30

US-08-776-585-17
; Sequence 17, Application US/08776585
; Patent No. 5932426
; GENERAL INFORMATION:
; APPLICANT: BARALLE, Francesco E.
; APPLICANT: SCODELLER, Eduardo
; APPLICANT: TISMINETSKY, Sergio
; TITLE OF INVENTION: MOLECULAR PRESENTING SYSTEM
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,585
; FILING DATE: 31-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/03114
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 69592/106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5599
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-776-585-17

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 31
US-08-467-881A-98
; Sequence 98, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,881A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-881A-98

Query Match 100.0%; Score 35; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 32
US-09-289-942A-1
; Sequence 1, Application US/09289942A
; Patent No. 6482928
; GENERAL INFORMATION:
; APPLICANT: Pai, Emil F.
; APPLICANT: Klein, Michel H.
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Arthur
; TITLE OF INVENTION: Fab'-EPI TOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
; FILE REFERENCE: 1038-926 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/289,942A
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-09-289-942A-1

Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 33
US-09-873-459A-2
; Sequence 2, Application US/09873459A
; Patent No. 6627202
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-09-873-459A-2

Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 34

US-08-073-028-51
; Sequence 51, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073.028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-073-028-51

Query Match 100.0%; Score 35; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 35

US-09-071-877-15
; Sequence 15, Application US/09071877
; Patent No. 6015881
; GENERAL INFORMATION:
; APPLICANT: Kang, Myung-Chol
; APPLICANT: Bray, Brian
; APPLICANT: Lichty, Maynard
; APPLICANT: Mader, Catherine
; APPLICANT: Merutka, Gene
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS
; FILE REFERENCE: 7872-050
; CURRENT APPLICATION NUMBER: US/09/071.877
; CURRENT FILING DATE: 1998-05-01

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: fragment
US-09-071-877-15

Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 2 ELDKWA 7

RESULT 36

US-08-554-616-51
; Sequence 51, Application US/08554616
; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,616
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,028
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-554-616-51

Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

```

; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 434:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-474-349A-434

Query Match 100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 40
US-09-315-304B-219
; Sequence 219, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
;

Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

RESULT 39
US-08-474-349A-434
; Sequence 434, Application US/08474349A
;

US-09-082-279B-219
; Sequence 219, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-219

Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 38
US-09-045-920-15
; Sequence 15, Application US/09045920
; Patent No. 6281331
; GENERAL INFORMATION:
; APPLICANT: Kang, Myung-Chol
; APPLICANT: Bray, Brian
; APPLICANT: Lichty, Maynard
; APPLICANT: Mader, Catherine
; APPLICANT: Merutka, Gene
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS
; FILE REFERENCE: 7872-047
; CURRENT APPLICATION NUMBER: US/09/045,920
; CURRENT FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: fragment
; US-09-045-920-15

Query Match 100.0%; Score 35; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

RESULT 39
US-08-474-349A-434
; Sequence 434, Application US/08474349A
;

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-219

Query Match      100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 41
US-09-834-784-219
; Sequence 219, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-219

Query Match      100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 42
US-09-515-965A-219
; Sequence 219, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-219

Query Match      100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 43
US-09-515-965A-1664
; Sequence 1664, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1664
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-1664

Query Match      100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6

RESULT 44
US-09-350-641C-219
; Sequence 219, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
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;; PRIOR FILING DATE: 1999-05-20
;; PRIOR APPLICATION NUMBER: 09/082,279
;; PRIOR FILING DATE: 1998-05-20
;; NUMBER OF SEQ ID NOS: 1757
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 219
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Core polypeptide
US-09-350-641C-219

Query Match 100.0%; Score 35; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 45
US-08-073-028-52
; Sequence 52, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-073-028-52

Query Match 100.0%; Score 35; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 46
US-08-975-699-13
; Sequence 13, Application US/08975699
; Patent No. 5858369
; GENERAL INFORMATION:
; APPLICANT: MATSUO, KAZUHIRO
; APPLICANT: CHUJO, YOSHITOMO
; APPLICANT: YAMAZAKI, AKIHIRO
; APPLICANT: HONDA, MITSUO
; APPLICANT: YAMAKAZI, SHUDO
; APPLICANT: TASAKA, HIROMICHI
; TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
; TITLE OF INVENTION: VACCINE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,699
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/619,512
; FILING DATE: 29-MAR-1996
; APPLICATION NUMBER: PCT/JP95/01515
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 178462/1994
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-795-0X PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; STRAIN: HIV-1
US-08-975-699-13

Query Match 100.0%; Score 35; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 8 ELDKWA 13

RESULT 47
US-08-972-089-13
; Sequence 13, Application US/08972089
; Patent No. 5885580
; GENERAL INFORMATION:

APPLICANT: MATSUO, KAZUHIRO
APPLICANT: CHUJO, YOSHITOMO
APPLICANT: YAMAZAKI, AKIHIRO
APPLICANT: HONDA, MITSUO
APPLICANT: YAMAKAZI, SHUDO
APPLICANT: TASAKA, HIROMICHI
TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,089
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,699
FILING DATE:
APPLICATION NUMBER: PCT/JP95/01515
FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 178462/1994
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-795-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
STRAIN: HIV-1
US-08-972-089-13

Query Match 100.0%; Score 35; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 8 ELDKWA 13

RESULT 48
US-08-486-099-169
Sequence 169, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-486-099-169

Query Match 100.0%; Score 35; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7

RESULT 49
US-08-486-099-170
Sequence 170, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OM protein - protein search, using sw model

Run on: March 16, 2004, 09:16:31 ; Search time 34 Seconds
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Title: US-10-024-329-2

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications AA:*

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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	35	100.0	6	14	US-10-448-546-4
5	35	100.0	6	15	US-10-283-403-12
6	35	100.0	6	15	US-10-369-121-53
7	35	100.0	7	9	US-09-873-459A-2
8	35	100.0	7	14	US-10-448-546-2
9	35	100.0	10	10	US-09-931-325A-132
10	35	100.0	10	10	US-09-930-915A-173
11	35	100.0	10	14	US-10-200-708-31
12	35	100.0	10	14	US-10-200-708-404
13	35	100.0	10	14	US-10-200-708-456
14	35	100.0	10	14	US-10-200-708-477
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138	35	100.0	35	14	US-10-252-136-17	Sequence 17, Appl	211	35	100.0	36	14	US-10-351-641-557	Sequence 557, Appl
139	35	100.0	35	14	US-10-351-641-48	Sequence 48, Appl	212	35	100.0	36	14	US-10-351-641-558	Sequence 558, Appl
140	35	100.0	35	14	US-10-351-641-376	Sequence 376, Appl	213	35	100.0	36	14	US-10-351-641-559	Sequence 559, Appl
141	35	100.0	35	14	US-10-351-641-544	Sequence 544, Appl	214	35	100.0	36	14	US-10-351-641-561	Sequence 561, Appl
142	35	100.0	35	14	US-10-351-641-636	Sequence 636, Appl	215	35	100.0	36	14	US-10-351-641-562	Sequence 562, Appl
143	35	100.0	35	14	US-10-351-641-638	Sequence 638, Appl	216	35	100.0	36	14	US-10-351-641-563	Sequence 563, Appl
144	35	100.0	35	14	US-10-351-641-795	Sequence 795, Appl	217	35	100.0	36	14	US-10-351-641-564	Sequence 564, Appl
145	35	100.0	35	14	US-10-351-641-799	Sequence 799, Appl	218	35	100.0	36	14	US-10-351-641-565	Sequence 565, Appl
146	35	100.0	35	14	US-10-351-641-1467	Sequence 1467, Appl	219	35	100.0	36	14	US-10-351-641-566	Sequence 566, Appl
147	35	100.0	35	15	US-10-005-305-33	Sequence 33, Appl	220	35	100.0	36	14	US-10-351-641-567	Sequence 567, Appl
148	35	100.0	35	15	US-10-005-305-66	Sequence 66, Appl	221	35	100.0	36	14	US-10-351-641-568	Sequence 587, Appl
149	35	100.0	36	9	US-09-796-202-10	Sequence 10, Appl	222	35	100.0	36	14	US-10-351-641-603	Sequence 603, Appl
150	35	100.0	36	9	US-09-779-451-5	Sequence 5, Appl	223	35	100.0	36	14	US-10-351-641-624	Sequence 624, Appl
151	35	100.0	36	9	US-09-779-451-47	Sequence 47, Appl	224	35	100.0	36	14	US-10-351-641-625	Sequence 625, Appl
152	35	100.0	36	9	US-09-779-451-50	Sequence 50, Appl	225	35	100.0	36	14	US-10-351-641-628	Sequence 628, Appl
153	35	100.0	36	9	US-09-779-451-56	Sequence 56, Appl	226	35	100.0	36	14	US-10-351-641-629	Sequence 629, Appl
154	35	100.0	36	9	US-09-912-824-1	Sequence 1, Appl	227	35	100.0	36	14	US-10-351-641-630	Sequence 630, Appl
155	35	100.0	36	9	US-09-834-628-1	Sequence 1, Appl	228	35	100.0	36	14	US-10-351-641-631	Sequence 631, Appl
156	35	100.0	36	9	US-09-854-816-1	Sequence 1, Appl	229	35	100.0	36	14	US-10-351-641-642	Sequence 642, Appl
157	35	100.0	36	9	US-09-854-816-108	Sequence 108, Appl	230	35	100.0	36	14	US-10-351-641-643	Sequence 643, Appl
158	35	100.0	36	9	US-09-874-475-16	Sequence 16, Appl	231	35	100.0	36	14	US-10-351-641-644	Sequence 644, Appl
159	35	100.0	36	10	US-09-493-346-1	Sequence 1, Appl	232	35	100.0	36	14	US-10-351-641-705	Sequence 705, Appl
160	35	100.0	36	14	US-10-116-797-1	Sequence 1, Appl	233	35	100.0	36	14		
161	35	100.0	36	14	US-10-252-136-1	Sequence 1, Appl	234	35	100.0	36	14		

235	35	100.0	36	14	US-10-351-641-719	Sequence 719, App	308	37	10	US-09-848-616-176	Sequence 176, App
236	35	100.0	36	14	US-10-351-641-720	Sequence 720, App	309	37	14	US-10-347-562-1	Sequence 1, Appli
237	35	100.0	36	14	US-10-351-641-721	Sequence 721, App	310	37	14	US-10-278-364A-8	Sequence 8, Appli
238	35	100.0	36	14	US-10-351-641-722	Sequence 722, App	311	35	100.0	US-10-351-641-771	Sequence 771, App
239	35	100.0	36	14	US-10-351-641-723	Sequence 723, App	312	35	100.0	US-10-351-641-775	Sequence 775, App
240	35	100.0	36	14	US-10-351-641-730	Sequence 730, App	313	35	100.0	US-10-351-641-905	Sequence 905, App
241	35	100.0	36	14	US-10-351-641-731	Sequence 731, App	314	35	100.0	US-10-086-409A-3	Sequence 3, Appli
242	35	100.0	36	14	US-10-351-641-748	Sequence 748, App	315	38	14	US-10-351-641-762	Sequence 762, App
243	35	100.0	36	14	US-10-351-641-749	Sequence 749, App	316	38	14	US-10-351-641-772	Sequence 772, App
244	35	100.0	36	14	US-10-351-641-752	Sequence 752, App	317	38	14	US-10-351-641-776	Sequence 776, App
245	35	100.0	36	14	US-10-351-641-753	Sequence 753, App	318	38	14	US-10-351-641-780	Sequence 780, App
246	35	100.0	36	14	US-10-351-641-754	Sequence 754, App	319	38	14	US-10-351-641-1509	Sequence 1509, Ap
247	35	100.0	36	14	US-10-351-641-755	Sequence 755, App	320	39	14	US-10-252-136-30	Sequence 30, Appl
248	35	100.0	36	14	US-10-351-641-756	Sequence 756, App	321	35	100.0	US-10-351-641-517	Sequence 517, App
249	35	100.0	36	14	US-10-351-641-757	Sequence 757, App	322	35	100.0	US-10-351-641-602	Sequence 602, App
250	35	100.0	36	14	US-10-351-641-758	Sequence 758, App	323	35	100.0	US-10-351-641-632	Sequence 632, App
251	35	100.0	36	14	US-10-351-641-834	Sequence 834, App	324	35	100.0	US-10-351-641-773	Sequence 773, App
252	35	100.0	36	14	US-10-351-641-856	Sequence 856, App	325	35	100.0	US-10-351-641-777	Sequence 777, App
253	35	100.0	36	14	US-10-351-641-1051	Sequence 1051, Ap	326	35	100.0	US-10-351-641-1503	Sequence 1503, Ap
254	35	100.0	36	14	US-10-351-641-1076	Sequence 1076, Ap	327	35	100.0	US-09-854-816-113	Sequence 113, App
255	35	100.0	36	14	US-10-351-641-1121	Sequence 1121, Ap	328	35	100.0	US-10-351-641-774	Sequence 774, App
256	35	100.0	36	14	US-10-351-641-1161	Sequence 1161, Ap	329	35	100.0	US-10-351-641-778	Sequence 778, App
257	35	100.0	36	14	US-10-351-641-1248	Sequence 1248, Ap	330	35	100.0	US-10-351-641-781	Sequence 781, App
258	35	100.0	36	14	US-10-351-641-1249	Sequence 1249, Ap	331	35	100.0	US-10-283-403-13	Sequence 13, Appl
259	35	100.0	36	14	US-10-351-641-1250	Sequence 1250, Ap	332	35	100.0	US-10-351-641-640	Sequence 640, App
260	35	100.0	36	14	US-10-351-641-1356	Sequence 1356, Ap	333	35	100.0	US-10-231-494-16	Sequence 16, Appl
261	35	100.0	36	14	US-10-351-641-1357	Sequence 1357, Ap	334	35	100.0	US-10-351-641-746	Sequence 746, App
262	35	100.0	36	14	US-10-351-641-1358	Sequence 1358, Ap	335	35	100.0	US-10-351-641-999	Sequence 999, App
263	35	100.0	36	14	US-10-351-641-1359	Sequence 1359, Ap	336	35	100.0	US-10-283-403-11	Sequence 11, Appl
264	35	100.0	36	14	US-10-351-641-1425	Sequence 1425, Ap	337	35	100.0	US-10-086-409A-6	Sequence 6, Appli
265	35	100.0	36	14	US-10-351-641-1469	Sequence 1469, Ap	338	35	100.0	US-09-779-451-41	Sequence 41, Appl
266	35	100.0	36	14	US-10-351-641-1470	Sequence 1470, Ap	339	35	100.0	US-09-779-451-45	Sequence 45, Appl
267	35	100.0	36	14	US-10-351-641-1475	Sequence 1475, Ap	340	35	100.0	US-09-779-451-48	Sequence 48, Appl
268	35	100.0	36	14	US-10-351-641-1476	Sequence 1476, Ap	341	35	100.0	US-09-779-451-54	Sequence 54, Appl
269	35	100.0	36	14	US-10-351-641-1477	Sequence 1477, Ap	342	35	100.0	US-09-854-816-109	Sequence 109, App
270	35	100.0	36	14	US-10-351-641-1478	Sequence 1478, Ap	343	35	100.0	US-09-854-816-112	Sequence 112, App
271	35	100.0	36	14	US-10-351-641-1479	Sequence 1479, Ap	344	35	100.0	US-10-438-691-2	Sequence 2, Appli
272	35	100.0	36	14	US-10-351-641-1482	Sequence 1482, Ap	345	35	100.0	US-10-158-742A-15	Sequence 15, Appl
273	35	100.0	36	14	US-10-351-641-1483	Sequence 1483, Ap	346	35	100.0	US-10-351-641-45	Sequence 45, Appl
274	35	100.0	36	14	US-10-351-641-1484	Sequence 1484, Ap	347	35	100.0	US-10-252-136-13	Sequence 13, Appl
275	35	100.0	36	14	US-10-351-641-1485	Sequence 1485, Ap	348	35	100.0	US-10-000-321-11	Sequence 11, Appl
276	35	100.0	36	14	US-10-351-641-1486	Sequence 1486, Ap	349	35	100.0	US-10-040-349B-2	Sequence 2, Appli
277	35	100.0	36	14	US-10-351-641-1492	Sequence 1492, Ap	350	35	100.0	US-09-854-816-100	Sequence 100, App
278	35	100.0	36	14	US-10-351-641-1493	Sequence 1493, Ap	351	35	100.0	US-09-854-816-86	Sequence 86, Appl
279	35	100.0	36	14	US-10-351-641-1494	Sequence 1494, Ap	352	35	100.0	US-09-854-816-87	Sequence 87, Appl
280	35	100.0	36	14	US-10-351-641-1505	Sequence 1505, Ap	353	35	100.0	US-09-854-816-88	Sequence 88, Appl
281	35	100.0	36	14	US-10-351-641-1506	Sequence 1506, Ap	354	35	100.0	US-09-854-816-89	Sequence 89, Appl
282	35	100.0	36	14	US-10-351-641-1507	Sequence 1507, Ap	355	35	100.0	US-09-854-816-90	Sequence 90, Appl
283	35	100.0	36	14	US-10-351-641-1508	Sequence 1508, Ap	356	35	100.0	US-09-854-816-91	Sequence 91, Appl
284	35	100.0	36	14	US-10-351-641-1510	Sequence 1510, Ap	357	35	100.0	US-10-263-103-33	Sequence 33, Appl
285	35	100.0	36	14	US-10-351-641-1511	Sequence 1511, Ap	358	35	100.0	US-10-438-691-4	Sequence 4, Appli
286	35	100.0	36	14	US-10-351-641-1512	Sequence 1512, Ap	359	35	100.0	US-10-000-321-11	Sequence 11, Appl
287	35	100.0	36	14	US-10-351-641-1514	Sequence 1514, Ap	360	35	100.0	US-10-263-103-25	Sequence 25, Appl
288	35	100.0	36	14	US-10-351-641-1515	Sequence 1515, Ap	361	35	100.0	US-10-438-691-8	Sequence 8, Appli
289	35	100.0	36	14	US-10-351-641-1516	Sequence 1516, Ap	362	35	100.0	US-10-059-271-84	Sequence 84, Appl
290	35	100.0	36	14	US-10-351-641-1517	Sequence 1517, Ap	363	35	100.0	US-10-059-271-81	Sequence 81, Appl
291	35	100.0	36	14	US-10-351-641-1518	Sequence 1518, Ap	364	35	100.0	US-09-854-816-49	Sequence 49, Appl
292	35	100.0	36	14	US-10-351-641-1519	Sequence 1519, Ap	365	35	100.0	US-09-854-816-50	Sequence 50, Appl
293	35	100.0	36	14	US-10-351-641-1520	Sequence 1520, Ap	366	35	100.0	US-10-059-271-82	Sequence 82, Appl
294	35	100.0	36	14	US-10-351-641-1749	Sequence 1749, Ap	367	35	100.0	US-10-059-271-97	Sequence 97, Appl
295	35	100.0	36	14	US-10-351-641-1750	Sequence 1750, Ap	368	35	100.0	US-09-854-816-38	Sequence 38, Appl
296	35	100.0	36	14	US-10-351-641-1751	Sequence 1751, Ap	369	35	100.0	US-09-854-816-7	Sequence 7, Appli
297	35	100.0	36	14	US-10-005-305-34	Sequence 34, Appl	370	35	100.0		
298	35	100.0	36	15	US-10-005-305-67	Sequence 67, Appl	371	35	100.0		
299	35	100.0	36	15	US-10-005-305-197	Sequence 197, Appl	372	35	100.0		
300	35	100.0	36	15	US-10-378-094-17	Sequence 17, Appl	373	35	100.0		
301	35	100.0	36	15	US-10-420-194-1233	Sequence 1233, Ap	374	35	100.0		
302	35	100.0	36	15	US-10-231-494-14	Sequence 14, Appl	375	35	100.0		
303	35	100.0	36	15			376	35	100.0		
304	35	100.0	36	15			377	35	100.0		
305	35	100.0	36	15			378	35	100.0		
306	35	100.0	36	15			379	35	100.0		
307	35	100.0	36	16			380	35	100.0		

381	35	100.0	268	9	US-09-854-816-8	Sequence 8, Appli	454	32	91.4	36	14	US-10-351-641-95	Sequence 95, Appl
382	35	100.0	268	9	US-09-854-816-9	Sequence 9, Appli	455	32	91.4	36	14	US-10-351-641-1223	Sequence 1223, Ap
383	35	100.0	268	9	US-09-854-816-10	Sequence 10, Appl	456	32	91.4	36	14	US-10-351-641-1361	Sequence 1361, Ap
384	35	100.0	268	9	US-09-854-816-11	Sequence 11, Appl	457	32	91.4	36	14	US-10-351-641-1444	Sequence 1444, Ap
385	35	100.0	268	9	US-09-854-816-12	Sequence 12, Appl	458	32	91.4	36	14	US-10-351-641-1449	Sequence 1449, Ap
386	35	100.0	268	9	US-09-854-816-13	Sequence 13, Appl	459	32	91.4	36	14	US-10-351-641-1450	Sequence 1450, Ap
387	35	100.0	268	9	US-09-854-816-14	Sequence 14, Appl	460	32	91.4	40	14	US-10-351-641-1447	Sequence 1447, Ap
388	35	100.0	268	9	US-09-854-816-15	Sequence 15, Appl	461	32	91.4	40	14	US-10-351-641-1448	Sequence 1448, Ap
389	35	100.0	268	9	US-09-854-816-16	Sequence 16, Appl	462	32	91.4	198	9	US-09-854-816-85	Sequence 85, Appl
390	35	100.0	268	9	US-09-854-816-17	Sequence 17, Appl	463	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
391	35	100.0	268	9	US-09-854-816-18	Sequence 18, Appl	464	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
392	35	100.0	268	9	US-09-854-816-19	Sequence 19, Appl	465	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
393	35	100.0	268	9	US-09-854-816-20	Sequence 20, Appl	466	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
394	35	100.0	268	9	US-09-854-816-21	Sequence 21, Appl	467	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
395	35	100.0	268	9	US-09-854-816-22	Sequence 22, Appl	468	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
396	35	100.0	268	9	US-09-854-816-23	Sequence 23, Appl	469	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
397	35	100.0	268	9	US-09-854-816-24	Sequence 24, Appl	470	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
398	35	100.0	268	9	US-09-854-816-25	Sequence 25, Appl	471	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
399	35	100.0	268	9	US-09-854-816-26	Sequence 26, Appl	472	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
400	35	100.0	268	9	US-09-854-816-27	Sequence 27, Appl	473	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
401	35	100.0	268	9	US-09-854-816-28	Sequence 28, Appl	474	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
402	35	100.0	268	9	US-09-854-816-29	Sequence 29, Appl	475	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
403	35	100.0	268	9	US-09-854-816-30	Sequence 30, Appl	476	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
404	35	100.0	268	9	US-09-854-816-31	Sequence 31, Appl	477	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
405	35	100.0	268	9	US-09-854-816-32	Sequence 32, Appl	478	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
406	35	100.0	268	9	US-09-854-816-33	Sequence 33, Appl	479	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
407	35	100.0	268	9	US-09-854-816-34	Sequence 34, Appl	480	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
408	35	100.0	268	9	US-09-854-816-35	Sequence 35, Appl	481	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
409	35	100.0	268	9	US-09-854-816-36	Sequence 36, Appl	482	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
410	35	100.0	268	9	US-09-854-816-37	Sequence 37, Appl	483	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
411	35	100.0	268	9	US-09-854-816-38	Sequence 38, Appl	484	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
412	35	100.0	268	9	US-09-854-816-39	Sequence 39, Appl	485	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
413	35	100.0	268	9	US-09-854-816-40	Sequence 40, Appl	486	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
414	35	100.0	268	9	US-09-854-816-41	Sequence 41, Appl	487	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
415	35	100.0	268	9	US-09-854-816-42	Sequence 42, Appl	488	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
416	35	100.0	268	9	US-09-854-816-43	Sequence 43, Appl	489	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
417	35	100.0	268	9	US-09-854-816-44	Sequence 44, Appl	490	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
418	35	100.0	268	9	US-09-854-816-45	Sequence 45, Appl	491	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
419	35	100.0	268	9	US-09-854-816-46	Sequence 46, Appl	492	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
420	35	100.0	268	9	US-09-854-816-47	Sequence 47, Appl	493	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
421	35	100.0	268	9	US-09-854-816-48	Sequence 48, Appl	494	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
422	35	100.0	268	9	US-09-854-816-49	Sequence 49, Appl	495	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
423	35	100.0	268	9	US-09-854-816-50	Sequence 50, Appl	496	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
424	35	100.0	268	9	US-09-854-816-51	Sequence 51, Appl	497	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
425	35	100.0	268	9	US-09-854-816-52	Sequence 52, Appl	498	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
426	35	100.0	268	9	US-09-854-816-53	Sequence 53, Appl	499	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
427	35	100.0	268	9	US-09-854-816-54	Sequence 54, Appl	500	32	91.4	269	9	US-09-854-816-29	Sequence 29, Appl
428	35	100.0	268	9	US-09-854-816-55	Sequence 55, Appl							
429	35	100.0	268	9	US-09-854-816-56	Sequence 56, Appl							
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433	35	100.0	268	9	US-09-854-816-60	Sequence 60, Appl							
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435	35	100.0	268	9	US-09-854-816-62	Sequence 62, Appl							
436	35	100.0	268	9	US-09-854-816-63	Sequence 63, Appl							
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445	35	100.0	268	9	US-09-854-816-72	Sequence 72, Appl							
446	35	100.0	268	9	US-09-854-816-73	Sequence 73, Appl							
447	35	100.0	268	9	US-09-854-816-74	Sequence 74, Appl							
448	35	100.0	268	9	US-09-854-816-75	Sequence 75, Appl							
449	35	100.0	268	9	US-09-854-816-76	Sequence 76, Appl							
450	35	100.0	268	9	US-09-854-816-77	Sequence 77, Appl							
451	35	100.0	268	9	US-09-854-816-78	Sequence 78, Appl							
452	35	100.0	268	9	US-09-854-816-79	Sequence 79, Appl							
453	35	100.0	268	9	US-09-854-816-80	Sequence 80, Appl							

ALIGNMENTS

RESULT 1

US-09-873-459A-4

; Sequence 4, Application US/09873459A

; Patent No. US20020064533A1

; GENERAL INFORMATION:

; APPLICANT: Murrav, Kenneth

; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC

; FILE REFERENCE: A067 CIP

; CURRENT APPLICATION NUMBER: US/09/873,459A

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: PCT/US99/28755

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: 60/110,911

; PRIOR FILING DATE: 1998-12-04

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus

;

;

;

US-09-873-459A-4.

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 2

US-10-041-414-7

; Sequence 7, Application US/10041414
; Publication No. US20030087225A1

; GENERAL INFORMATION:

; APPLICANT: SHIVER, JOHN W.

; DAVIES, MARY ELLEN

; FREED, DANIEL C.

; LIU, MARGARET A.

; PERRY, HELEN C.

; TITLE OF INVENTION: SYNTHETIC HIV ENV GENES

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.

; STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000

; CITY: RAHWAY

; STATE: NEW JERSEY

; COUNTRY: US

; ZIP: 07065-0907

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/041,414

; FILING DATE: 08-May-2002

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/802,368

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: HAND, J. MARK

; REGISTRATION NUMBER: 36,545

; REFERENCE/DOCKET NUMBER: 19643

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 732-594-3905

; TELEFAX: 732-594-4720

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-041-414-7

Query Match 100.0%; Score 35; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 3

US-10-024-329-2

; Sequence 2, Application US/10024329

; Publication No. US20030157063A1

; GENERAL INFORMATION:

; APPLICANT: SANHADJI, Kamel

; APPLICANT: TOURAINE, Jean-Louis

; APPLICANT: LEROY, Pierre

; APPLICANT: MEHTALI, Majid

; TITLE OF INVENTION: Gene therapy using anti-gp41 antibody and cd4 immunoadhesin

; FILE REFERENCE: 109993

; CURRENT APPLICATION NUMBER: US/10/024,329

; CURRENT FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 6

; TYPE: PRT

; ORGANISM: HIV-1 gp41 epitope

US-10-024-329-2

Query Match 100.0%; Score 35; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 4

US-10-448-546-4

; Sequence 4, Application US/10448546

; Publication No. US20030198649A1

; GENERAL INFORMATION:

; APPLICANT: Murray, Kenneth

; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC

; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS

; FILE REFERENCE: A067 CIP CON DIV 1

; CURRENT APPLICATION NUMBER: US/10/448,546

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: US/09/873,459

; PRIOR APPLICATION NUMBER: 2001-06-04

; PRIOR APPLICATION NUMBER: PCT/US99/28755

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: 60/110,911

; PRIOR FILING DATE: 1998-12-04

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus

US-10-448-546-4

Query Match 100.0%; Score 35; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 5

US-10-283-403-12

; Sequence 12, Application US/10283403

; Publication No. US20030219451A1

; GENERAL INFORMATION:

; APPLICANT: Kim, Peter S.

; APPLICANT: Sia, Samuel K.

; TITLE OF INVENTION: Stable Helical C Peptides and Uses

; FILE REFERENCE: Therefor

; FILE REFERENCE: 0399.2035-002

; CURRENT APPLICATION NUMBER: US/10/283,403

; CURRENT FILING DATE: 2002-10-29

; PRIOR APPLICATION NUMBER: US 60/350,099
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/334,528
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Core epitope for the 2F5 monoclonal antibody
US-10-283-403-12

Query Match 100.0%; Score 35; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 6
US-10-369-121-53
; Sequence 53, Application US/10369121
; Publication No. US2003029214A1
; GENERAL INFORMATION:
; APPLICANT: SHIVER, JOHN W.
; LIU, MARGARET A.
; PERRY, HELEN C.
; DAVIES, MARY-ELLEN M.
; FREED, DANIEL C.

; TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0907

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/369,121
; FILING DATE: 17-Feb-2003
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,798A
; FILING DATE: 28-Jun-1999
; APPLICATION NUMBER: US/08/877,418
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19729Y

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-369-121-53

Query Match 100.0%; Score 35; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 7
US-09-873-459A-2
; Sequence 2, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT FILING DATE: 2001-09-17
; CURRENT APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-873-459A-2

Query Match 100.0%; Score 35; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 8
US-10-448-546-2
; Sequence 2, Application US/10448546
; Publication No. US20030198649A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP CON DIV 1
; CURRENT APPLICATION NUMBER: US/10/448,546
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/873,459
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-448-546-2

Query Match 100.0%; Score 35; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

```

RESULT 9
US-09-931-325A-132
; Sequence 132, Application US/09931325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931.325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US/09/931.325A
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-931-325A-132

Query Match      100.0%; Score 35; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      3 ELDKWA 8

RESULT 10
US-09-930-915A-173
; Sequence 173, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930.915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 173
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-930-915A-173

Query Match      100.0%; Score 35; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      3 ELDKWA 8

RESULT 11
US-10-200-708-31
; Sequence 31, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001

```

```

; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-31

Query Match      100.0%; Score 35; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      1 ELDKWA 6

RESULT 12
US-10-200-708-404
; Sequence 404, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 404
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-404

Query Match      100.0%; Score 35; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
Db      2 ELDKWA 7

RESULT 13
US-10-200-708-456
; Sequence 456, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036

```

; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 456
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-456

Query Match 100.0%; Score 35; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7
|||||

RESULT 14

US-10-200-708-477
; Sequence 477, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 477
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-477

Query Match 100.0%; Score 35; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 2 ELDKWA 7
|||||

RESULT 15

US-10-351-641-219
; Sequence 219, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M. D.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641

; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 219
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-219

Query Match 100.0%; Score 35; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 16

US-10-005-305-43
; Sequence 43, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-43

Query Match 100.0%; Score 35; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 1 ELDKWA 6
|||||

RESULT 17

US-10-005-305-88
; Sequence 88, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1

; CURRENT APPLICATION NUMBER: US/10/005,305
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-88

Query Match 100.0%; Score 35; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 ELDKWA 6
| | | | |
Db 1 ELDKWA 6

RESULT 18
US-10-252-136-22
; Sequence 22, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-22

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 19
US-10-252-136-23
; Sequence 23, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-23

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 20
US-10-252-136-24
; Sequence 24, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-24

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Qy 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 21
US-10-252-136-25
; Sequence 25, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-25

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 22
US-10-252-136-26
; Sequence 26, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-26

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 23
US-10-351-641-218
; Sequence 218, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-218

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 24
US-10-351-641-267
; Sequence 267, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 267
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-267

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
| | | | |
Db 2 ELDKWA 7

RESULT 25
US-10-351-641-268
; Sequence 268, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 268
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-10-351-641-268

Query Match 100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-268

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 26
US-10-351-641-269
; Sequence 269, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 269
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-269

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 27
US-10-351-641-270
; Sequence 270, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
```

```
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 270
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-270

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 28
US-10-351-641-530
; Sequence 530, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-530

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 29
US-10-351-641-531
; Sequence 531, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
```

```
; CURRENT APPLICATION NUMBER: US/10/351.641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350.641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315.304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082.279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-531

Query Match      100.0%; Score 35; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 30
US-10-005-305-44
; Sequence 44, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005.305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132.686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-44

Query Match      100.0%; Score 35; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 31
US-10-005-305-87
; Sequence 87, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
US-10-005-305-87

; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005.305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 60/132.686
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 531
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-87

Query Match      100.0%; Score 35; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 2 ELDKWA 7

RESULT 32
US-09-931-325A-133
; Sequence 133, Application US/09931325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931.325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225.943
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGNED
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-931-325A-133

Query Match      100.0%; Score 35; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
   |||||
Db 6 ELDKWA 11

RESULT 33
US-09-930-915A-174
; Sequence 174, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930.915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226.867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225.843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; 
```



```
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-86

Query Match          100.0%; Score 35; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 3 ELDKWA 8

RESULT 38
US-09-810-310-41
; Sequence 41, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Bezofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIIGEN
US-09-810-310-41

Query Match          100.0%; Score 35; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 6 ELDKWA 11

RESULT 39
US-10-252-136-19
; Sequence 19, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-19

Query Match          100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 3 ELDKWA 8

RESULT 40
US-10-252-136-20
; Sequence 20, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-20

Query Match          100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 3 ELDKWA 8

RESULT 41
US-10-252-136-21
; Sequence 21, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-21

Query Match          100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 ELDKWA 6
    |||||
Db 3 ELDKWA 8

RESULT 42
US-10-351-641-216
; Sequence 216, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 216
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-216

Query Match 100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 4 ELDKWA 9

RESULT 43
US-10-351-641-372
; Sequence 372, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-372

Query Match 100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 3 ELDKWA 8

RESULT 44
US-10-351-641-373
; Sequence 373, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-373

Query Match 100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 3 ELDKWA 8

RESULT 45
US-10-351-641-374
; Sequence 374, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-374
```

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; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-372

Query Match 100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 3 ELDKWA 8

RESULT 44
US-10-351-641-373
; Sequence 373, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-373

Query Match 100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
    |||||
Db 3 ELDKWA 8

RESULT 45
US-10-351-641-374
; Sequence 374, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-374
```

```
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-374

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
       |||||
Db      3 ELDKWA 8

RESULT 46
US-10-351-641-513
; Sequence 513, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 513
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-513

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
       |||||
Db      3 ELDKWA 8

RESULT 47
US-10-351-641-514
; Sequence 514, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 514
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-514

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
       |||||
Db      3 ELDKWA 8

RESULT 48
US-10-351-641-515
; Sequence 515, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 515
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-515

Query Match      100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELDKWA 6
       |||||
Db      3 ELDKWA 8

RESULT 49
US-10-351-641-792
; Sequence 792, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
```

; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 792
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-792

Query Match 100.0%; Score 35; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 4 ELDKWA 9

RESULT 50
US-10-005-305-46
; Sequence 46, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-46

Query Match 100.0%; Score 35; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 4 ELDKWA 9

Search completed: March 16, 2004, 09:19:33
Job time : 35 secs

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